

101500240

FIGURE 1

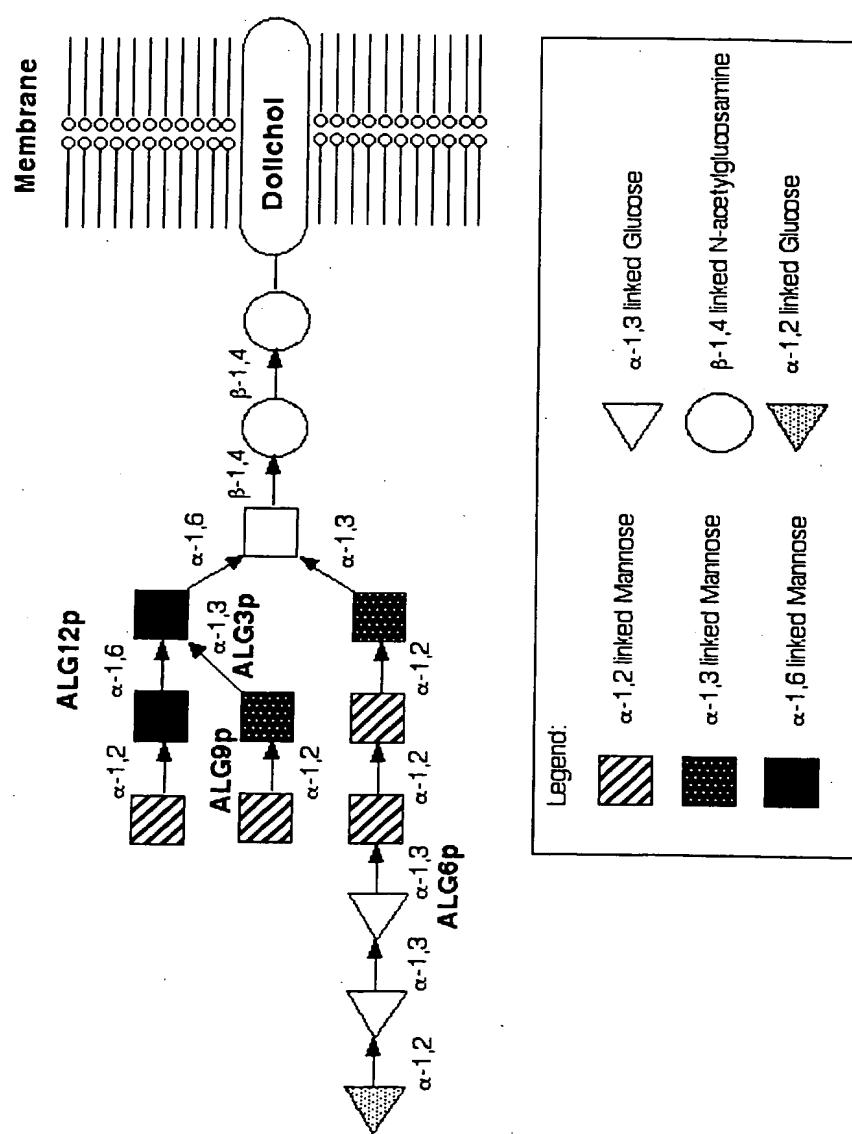
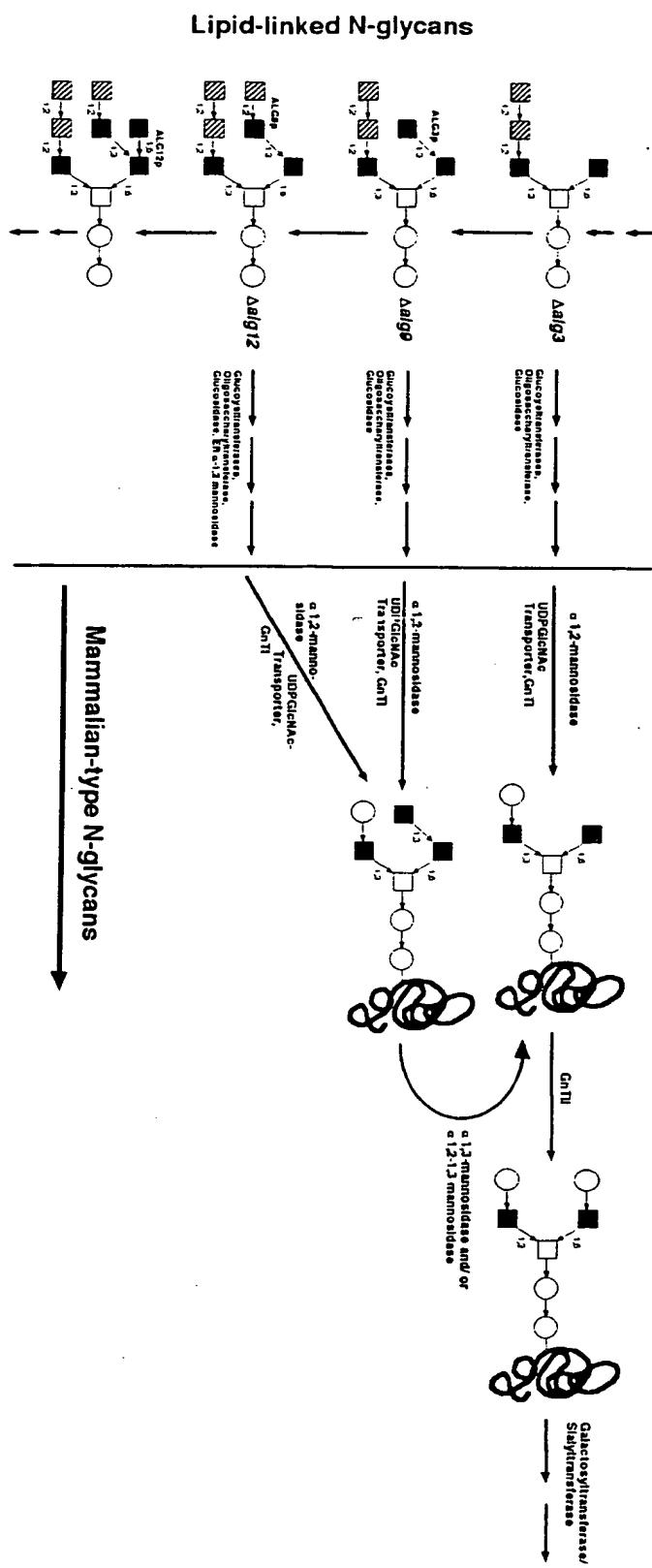


FIGURE 2



10/500240

FIGURE 3

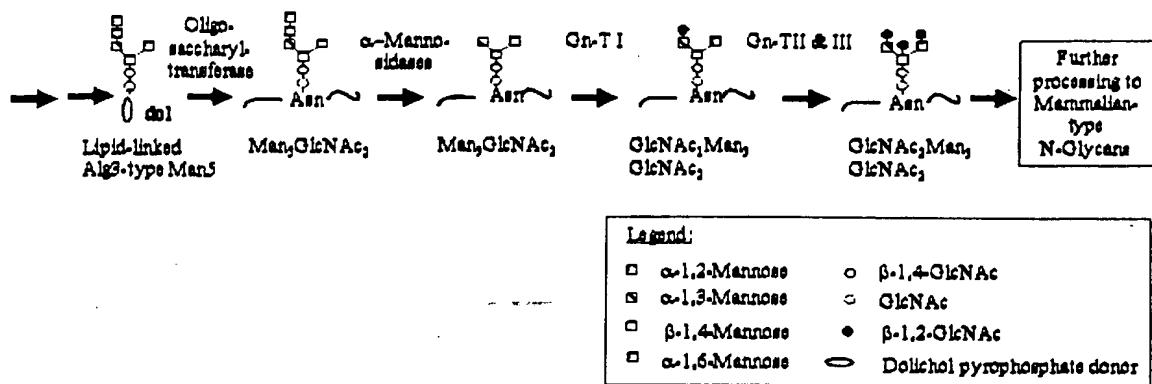


FIGURE 4 (sheet 1)

ALG3 Blast 05-22-01

Sequences producing significant alignments:	(bits) Value
gi 586444 sp P38179 ALG3_YEAST DOLICHYL-P-MAN:MAN(5)GLCNAC(...	797 0.0
gi 3024226 sp Q92685 ALG3_HUMAN DOLICHYL-P-MAN:MAN(5)GLCNAC...	173 7e-43
gi 3024221 sp Q24332 NT56_DROVI LETHAL(2)NEIGHBOUR OF TID P...	145 3e-34
gi 3024222 sp Q27333 NT56_DROME LETHAL(2)NEIGHBOUR OF TID P...	121 3e-27
gi 10720153 sp P82149 NT53_DROME LETHAL(2)NEIGHBOUR OF TID ...	121 5e-27
gi 1707982 sp P40989 GLS2_YEAST 1,3-BETA-GLUCAN SYNTHASE CO...	32 2.8
gi 1346146 sp P38631 GLS1_YEAST 1,3-BETA-GLUCAN SYNTHASE CO...	31 6.6

Alignments

Yeast

>gi|586444|sp|P38179|ALG3_YEAST DOLICHYL-P-MAN:MAN(5)GLCNAC(2)-PP-DOLICHYL MANNOSYLTRANSFERASE
(DOL-P-MAN DEPENDENT ALPHA(1-3)-MANNOSYLTRANSFERASE)
(HM-1 KILLER TOXIN RESISTANCE PROTEIN)
Length = 458

Score = 797 bits (2059), Expect = 0.0
Identities = 422/458 (92%), Positives = 422/458 (92%)

Query: 1	MEGEQSPQGEKSLQRKQFVRPPLDLWQDLKDGVRYVI FDCRANLIVMPLLILFESMLCKI	60
Sbjct: 1	MEGEQSPQGEKSLQRKQFVRPPLDLWQDLKDGVRYVI FDCRANLIVMPLLILFESMLCKI	60
Query: 61	IIKKVAYTEIDYKAYMEQIEMIQLDGMLDYSQVSGGTGPLVYPAGHVLIYKMMYWLT	120
Sbjct: 61	IIKKVAYTEIDYKAYMEQIEMIQLDGMLDYSQVSGGTGPLVYPAGHVLIYKMMYWLT	120
Query: 121	DHVERGQVFYRLYLLTLALQMACYYLLHPPCVVLACLSKRLHSIYVLRFLND	180
Sbjct: 121	DHVERGQVFYRLYLLTLALQMACYYLLHPPCVVLACLSKRLHSIYVLRFLND	180
Query: 181	FMVVTVLGAIVASRCHQRPKLKSLALVISATYSMAVSIMNALLYFPAMMISLFIL	240
Sbjct: 181	FMVVTVLGAIVASRCHQRPKLKSLALVISATYSMAVSIMNALLYFPAMMISLFIL	240
Query: 241	NVILTLDDLVAMIAWQAVAVPFPLRSFPQQYLCAFNFGRKFMYQWSINWQMD	300
Sbjct: 241	NVILTLDDLVAMIAWQAVAVPFPLRSFPQQYLCAFNFGRKFMYQWSINWQMD	300
Query: 301	KRFXXXXXXXXXXXXXXFVTRYPRILPDWLSSLCHPLRKNAVLNANPAKTIPFV	360
KRF	FVTRYPRILPDWLSSLCHPLRKNAVLNANPAKTIPFV	360
Sbjct: 301	KRFHLALLISHLIALTTLFVTRYPRILPDWLSSLCHPLRKNAVLNANPAKTIPFV	360
Query: 361	FIGVLFSRSLHYQFLSWYHWTLPILIFWSGMPFFVGPIWYVLHEWCWNSYPPNSQ	420
Sbjct: 361	FIGVLFSRSLHYQFLSWYHWTLPILIFWSGMPFFVGPIWYVLHEWCWNSYPPNSQ	420
Query: 421	XXXXXXXXXXXXXXXXXSGSVALAKSHLRTTSSMEKKLN	458
SGSVALAKSHLRTTSSMEKKLN		
Sbjct: 421	LALNTVLLLLALTQLSGSVALAKSHLRTTSSMEKKLN	458

FIGURE 4 (sheet 2)

Human

```

>gi|3024226|sp|Q92685|ALG3_HUMAN DOLICHYL-P-MAN:MAN(5)GLCNAC(2)-PP-DOLICHYL
MANNOSYLTRANSFERASE
(DOL-P-MAN DEPENDENT ALPHA(1-3)-MANNOSYLTRANSFERASE)
(NOT56-LIKE PROTEIN)
Length = 438

Score = 173 bits (439), Expect = 7e-43
Identities = 133/396 (33%), Positives = 195/396 (48%), Gaps = 28/396 (7%)

Query: 26 WQDLKDGVRVIFDCRANLIVMPPLLILFESMLCKIIKKVAYTEIDYKAYMEQIEMIQLD 85
WQ+ R ++ + R L+V L L E + +I +VAYTEID+KAYM ++E + ++
Sbjct: 29 WQER---RLLLREPRYTLLVAACLCLAEVGITFWVIHRVAYTEIDWKAYMAEVEGV-IN 83

Query: 86 GMMLDSQVSGGTGPLVYPAGHVLIYKMMYWLTGMDHVERGQVFFRYLYLLTLALQMACY 145
G DY+Q+ G TGPLVYPAG V I+ +Y+ T + Q F LYL TL L .Y
Sbjct: 84 GTYDYTQLQGDTGPLVYPAGFVYIFMGLYYATSRGTDIRMAQNI FAVLYLATLLLVFLIY 143

Query: 146 Y-LLHLPPWC-VVLACLSKRLHSIYVLRFLNDCFTTLMVVTVLGAIVASRCHQRPKLKK 203
+ +PP+ + C S R+HSI+VRLRFND + + +L + OR
Sbjct: 144 HQTCKVPPFVFFFMCASYRVHSIFVRLFNDP----VAMVLLFLSINLLAQRWGWG- 197

Query: 204 SLALVISATYSMAVSIKMNALLYFPAMMISLFILNDANVILTLDDLVAMIAWQAVAVPF 263
+ S+AVS+KMN LL+ P ++ L L L + A + QV + +PF
Sbjct: 198 -----CCFFSLAVSVKMNVLLFAPGLFLLLTQFGFRGALPKLGICAGL--QVVLGLPF 249

Query: 264 LRSFPQQYLHCAFNFGRKFMYQWSINWQMMDEEA FNDKRFXXXXXXXXXXXXFVTRY 323
L P YL +F+ GR+F++ W++NW+ + E F + F + R+
Sbjct: 250 LLENPSGYLSRSFDLGRQFLFHWTVNWRFLPEALFLHRAFHLLTAHTLFLFALCRW 309

Query: 324 PRILPDWLSSLCHPLRKNAVLNANPAKTI PFLIASNFVLFSLHYQFLSWYHWTLP 383
R + S L P ++ I L SNFIG+ FSRSLHYQF WY TLP
Sbjct: 310 HRTGESILSLLRDPSKRKVPPQPLTPNQIVSTLFTSNFIGICFSRSLHYQFYVWYFHTLP 369

Query: 384 ILIF----WSGMPPFFVGPIWYVLHEWCNSYPPNS 414
L++ W + + + E WN+YP S
Sbjct: 370 YLLWAMPARWLTHLLRLLVGLI--ELSWNTYPSTS 403

```

Drosophila Vi

```

>gi|3024221|sp|Q24332|NT56_DROVI LETHAL(2)NEIGHBOUR OF TID PROTEIN (NOT58)
Length = 526

Score = 145 bits (366), Expect = 3e-34
Identities = 103/273 (37%), Positives = 157/273 (56%), Gaps = 17/273 (6%)

Query: 33 VRYVIFDCRANLIVMPPLLILFESMLCKIIKKVAYTEIDYKAYMEQIEMIQLDGMLDYSQ 92
++Y+ F+ A IV L++L E+++ ++I++V YTEID+KAYM++ E L+G +YS
Sbjct: 34 IKYLAPEPAALPIVSVLIVLAEAVINV LVIQRPVYTEIDWKAYMCECEGF-LNGTTNYSL 92

Query: 93 VSGGTGPLVYPAGHVLIYKMMYWLTGMDHVERGQVFFRYLYLLTLALQMACYLLH- LP 151
+ G TGPLVYP A V IY +Y+LT +V Q F +YLL + L + Y +P
Sbjct: 93 LRGDTGPLVYPAAFVYIYSGLYYLTGQGTNVRLAQYIFACIYLLQMCLVRLYTKSRKVP 152

Query: 152 PWCVVLACL-SKRLHSIYVLRFLNDCFTTLMVVTVLGAIVASRCHQRPKLKKSLALVIS 210
P+ +VL+ S R+HSIYVRLFND L +L A + QR L S
Sbjct: 153 PYVLVLSAFTSYRIHSIYVRLFNDPVAIL-----LLYAALNLFLDQRWTLG-----S 200

Query: 211 ATYSMAVSIKMNALLYFPAMMISLFILNDANVILTLDDLVAMIAWQAVAVPFLRSFPQQ 270
YS+AV +KMN + A + LF L + V+ TL+ L Q+ + PFLR+ P +
Sbjct: 201 ICYSLAVGVKMN--ILLFAPALLFYLANLGVLRTLVLQLTICAVLQLFIGAPFLRTHPM 258

```

10/500240

FIGURE 4 (sheet 3)

Query: 271 YLHCAFNFGRKFMYQWSINWQMMDEEAFNDKRF 303
YL +F+ GR F ++W++N++ + +E F + F
Sbjct: 259 YLRGSFDLGRIFEHKWTVNYRFLSKELFEQREF 291

Score = 53.3 bits (127), Expect = 1e-06
Identities = 31/62 (50%), Positives = 41/62 (66%), Gaps = 6/62 (9%)

Query: 352 IPFVLIASNFIGVLSRSLHYQFLSWYHWTLPIIWFSGMPFFVGPIWYVLH--EWCWNS 409
+PF L NFIGV +RSLHYQF WY +LP L+ WS P+ +G + +L E+CWN+
Sbjct: 412 LPFFL--CNFIGVACARSLHYQFYIWYFHSLPYLV-WS-TPYSLGVRYLILGLIEYCWNT 467

Query: 410 YP 411
YP
Sbjct: 468 YP 469

Drosophila melanogaster

>gi|3024222|sp|Q27333|NT56_DROME LETHAL(2)NEIGHBOUR OF TID PROTEIN (NOT56)
(NOT45)
Length = 510

Score = 121 bits (305), Expect = 3e-27
Identities = 96/272 (35%), Positives = 154/272 (56%), Gaps = 17/272 (6%)

Query: 34 RYVIFDCRANLIVMPPLLILFESMLCKIIKKVAYTEIDYKAYMEQIEMIQLDGMQLDYSQV 93
+Y++ + A IV ++L E ++ ++I++VYTEID+ AYM++ E L+G +YS +
Sbjct: 36 KYLLLEPAALPIVGLFVLLAELVINVVVIQRVPYTEIDWVAYMQECEGF-LNGTTNYSLL 94

Query: 94 SGGTGPLVYPAGHVLIYKMMYWLTGMDHVERGQVFFRYLYLLTLALQMACYYLLH-LPP 152
G TGPLVYPA V IY +Y++T +V Q F +YLL LAL + Y +PP
Sbjct: 95 RGDTGPLVYPAAFVYIYSALYYVTSHGTNVRLAQYIFAGIYLLQLALVRLY SKSRKVPP 154

Query: 153 WCVVLACL-SKRLHSIYVLRFLNDCFTTLMVVTVLGAIVASRCHQRPKLKSSLALVISA 211
+ +VL+ S R+HSIYVLRLFND + V +L A + +R L S
Sbjct: 155 YVLVLSAFTSYRIHSIYVLRLFNDP-----VAVLLLYAALNLFLDRRWTLG-----ST 202

Query: 212 TYSMAVSIKMNALLYFPAMMISLFIILNDANVILTLLDLVAMIAWQVAVAVPFLRSFPQQY 271
+S+AV +KMN + A + LF L + ++T+L L Q+ + PFL + P +Y
Sbjct: 203 FFSLAVGVKMN--ILLFAPALLLFYLANLGLRTILQLAVCGVIQLLLGAPFLLTHPVEY 260

Query: 272 LHCAFNFGRKFMYQWSINWQMMDEEAFNDKRF 303
L +F+ GR F ++W++N++ + +F ++F
Sbjct: 261 LRGSFDLGRIFEHKWTVNYRFLSRDVFENRTF 292

Score = 49.4 bits (117), Expect = 2e-05
Identities = 27/60 (45%), Positives = 35/60 (58%), Gaps = 2/60 (3%)

Query: 352 IPFVLIASNFIGVLSRSLHYQFLSWYHWTLPIIWFSGMPFFVGPIWYVLHHEWCWNSYP 411
+PF L N +GV SRSLHYQF WY +LP L + + V + L E+CWN+YP
Sbjct: 407 LPFFL--CNLGVGVACSRSLHYQFYIWYFHSLPYLAWSPTYSLGVRCILGLIEYCWNTYP 464

10/500240

FIGURE 4 (sheet 4)

Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Hits to DB: 28883317
Number of Sequences: 96469
Number of extensions: 1107545
Number of successful extensions: 2870
Number of sequences better than 10.0: 16
Number of HSP's better than 10.0 without gapping: 5
Number of HSP's successfully gapped in prelim test: 11
Number of HSP's that attempted gapping in prelim test: 2839
Number of HSP's gapped (non-prelim): 23

length of query: 458
length of database: 35,174,128
effective HSP length: 45
effective length of query: 413
effective length of database: 30,833,023
effective search space: 12734038499
effective search space used: 12734038499
T: 11
A: 40
X1: 15 (7.1 bits)
X2: 38 (14.6 bits)
X3: 64 (24.7 bits)
S1: 40 (21.8 bits)
S2: 67 (30.4 bits)

10/500240

FIGURE 5

S. cerevisiae ALG3

ATGGAAGGTGAACAGTCTCCGCAAGGTAAAAGTCTCTGCAAAGGAAGC
AATTGTCAGACCTCCGCTGGATCTGGCAGGATCTCAAGGACGGTGTG
CGCTACGTGATCTCGATTGTAGGGCCAATCTTATCGTTATGCCCTTTG
ATTTGTCGAAAGCATGCTGTGCAAGATTATCATTAAAGAAGGTAGCTTAC
ACAGAGATCGATTACAAGGCATGGAGCAGATCGAGATGATTCACT
CGATGGCATGCTGGACTACTCTCAGGTGAGTGGTGGAACGGGCCGCTGG
TGTATCCAGCAGGCCACGTCTGATCTACAAGATGATGACTGGCTAAC
GAGGAATGGACCACGTTAGCGCGGGCAAGTGTGTTAGATACTTGTA
TCTCCTTACACTGGCGTTACAAATGGCGTGTACTACCTTTACATCTACC
ACCGTGGTGTGGTCTGGCGTGCCTCTCTAAAAGATTGCACTCTATT
CGTCTACGGTTATCAATGATTGCTTCACTACTTGTGTTATGGTCGTACG
GTTTGGGGCTATCGTGGCCAGCAGGTGCCATCAGCGCCCCAAATTAAA
GAAGTCCCTGCGCTGGTATCTCCGCAACATACAGTATGGCTGTGAGCA
TTAAGATGAATGCGCTGTTGATTCCCTGCAATGATGATTCTCTATT
CCTTAATGACGCGAACGTAATCCTACTTTGTTGGATCTCGTTGCGATGAT
TGCATGGCAAGTCGCAGTTGCAGTGCCTCCTGCGCAGCTTCCGCAACA
GTACCTGCATTGCGCTTTAATTCCGGCAGGAAGTTATGACCAATGGAG
TATCAATTGGCAAATGATGGATGAAGAGGGTTCAATGATAAGAGGTTCC
ACTTGGCCCTTTAATCAGCCACCTGATAGCGCTACCCACACTGTTCGTCA
CAAGATACCCTCGCATCCTGCCGATTATGGTCTCCCTGTGCCATCCGC
TGAGGAAAAATGCAGTGCTCAATGCCATCCGCAAGACTATTCCATT
GTTCTAATCGCATCCAACCTCATCGCGTCCTATTCAAGGTCCCTCCAC
TACCAAGTTCTATCCTGGTATCACTGGACTTGCCTATACTGATCTTG
CGGGAAATGCCCTCTCGTTGGCCATTGGTACGTCTGCACGAGTGGT
GCTGGAATTCTATCCACCAAACTCACAAGCAAGCACGCTATTGGCA
TTGAATACTGTTCTGTTGCTTCTATTGGCCTGACGCAGCTATCTGGT
TCGCCCTGCCAAAAGCCATCTCGTACCAACCAGCTATGGAAAAAAAG
CTCAACTGA

S. cerevisiae Alg3p

MEGEQSPQGEKSLQRKQFVRPLDLWQDLKDGVRYVIFDCRANLIVMPLLIL
FESMLCKIIKKVAYTEIDYKAYMEQIEMIQLDGMLDYSQVSGGTGPLVYPAG
HVLIYKMMYWLTEGMDHVERGQVFRLYLLTLALQMACYLLHLPPWC
VLACLSKRLHSIYVRLFNDCTTLMVVTVLGAIVASRCHQRPKLKKSLALV
ISATYSMAVSIMNALLYFPAMMISLFLINDANVILTLSDLVAMIAWQVA
VPFLRSFPQQYLHCAFNFGRKFMYQWSINWQMMDEEA
FNDKRFHLALLISHL
IALTTLFVTRYPRILPDLWSSLCHPLRKNAVLANPAKTIPFVLIASNFIGVLFS
RSLHYQFLSWYHWTLPIIFWSGMPFFVGPIWYVLHEWCWNSYPPNSQASTL
LLALNTVLLLLALTQLSGSVALAKSHLRTTSSMEKLN

10/500240

FIGURE 6

P. pastoris ALG3

ATGCCTCCGATAGAGCCAGCTGAAAGGCCAAGCTTACGCTGAAAAATGT
TATCGGTGATCTAGTGGCTCTTATTCAAAACGTTTATTAAACCCAGATTT
AGTGTCTTCGTTGCACCTCTTATGGTAGCTGATCCATTGTTATCAAGG
TGATCATTGGCACTGTTCCACACAGATATTGATTTCATATGCA
ACAAATCTTAAAATTCGACAAGGAGAATTAGATTATAGCAACATATTG
GTGACACCAGGTCCATTGGTTACCCAGCCGCCATGTTCATGCTTACTCAG
TACTTCGTGGTACAGTGATGGTGGAGAACGTCAGTTGTTCAACAA
GCATTGGTTGGTATACCTAGGTTGCTTACTATCCATCAGCTCCTACT
TTTCTCTGGCTTAGGGAAAATACCTCCGGTTATTGTTGTTGGTAGC
GTCCAAGAGACTGCATTCAATATTGTATTGAGACTCTTCAATGACTGTT
AACAAACATTTGATGTTGGCAACTATAATCATCCTCAACAAGCAAGTAG
CTGGAGGAAGATGGCACAACTATTCCATTATCTGTCCTGATGCTGCAG
ATACGTACAGTTAGCCATCTGTAAAGATGAATGCGCTGCTATAACCTCC
CAGCATTCTACTACTCATATATCTATTGACGAAAATTGATTAAAG
CCTTGGCACCTGTTAGTTGATATTGGTGCAGTACGCCATTCTTATAAGTGG
CGTTCAATTACCGTTGCACTATGATGATCAGGCAAATGAAATTGTTCTG
CCTACTTAGACAGGGCTTGACTTAGTCGCCATTCTTATAAGTGG
CGGTTAATTGGCGCTTTGAGCCAAGAACTTCACAAATGTCCATTTC
ACCAGCTCCTGTTGCTCTCCATATTACGTTAGTCTGTTCATCCTCAA
GTTCCTCTCTCCTAAAAACATTGGAAAACCGCTGGTAGATTGTGG
CATTTCAAATTGGAAGCCAACCTTATCTCCAACCAATTATCAACGA
CCCAGAAAGAAGCCCAGATTGTTACACCGTCATGGCTACTACCAACTT
AATAGGGGTGCTTTGCAAGATCTTACACTACCAGTCTTAAGCTGGTA
TGCCTCTCTTGCATATCTCCTTACAAGGCTCGTCTGAACCTTATAGCA
TCTATTATTGTTATGCCGCTCACGAGTATTGCTGGTTGGTCTTCCAGCTA
CAGAACAAAGTCCCGTTGGTATCTACTACTTATCCTGATT
TCATTTCACCAACAGTTATTCCCTCTCAATCGGTCCCTGCAGAAA
AAAAGAACATCAA

P. pastoris Alg3p

MPPIEPAERPKLTLKNVIGDLVALIQNVLNPDSVFVAPLLWLADSIVIKVIIG
TVSYTDIDFSSYMQQIFKIRQGELDYSNIFGDTGPLVYPAGHVHAYSVLSWYS
DGGEDVSFVQQAFGWLYLGCLLSISSYFFSGLGKIPPVYFVLLVASKRLHSIF
VRLFLNDCLTFMLLATIILQQASSWRKDGTIPLSVPDAADTYSLAISVKMN
ALLYLP AFLLIYLICDENLIKALAPVLVLILVQVGVGYSFILPLHYDDQANEIR
SAYFRQAFDFSRQFLYKWTVNWRFLSQETFNNVHFHQLLFALHIITLVLFILKF
LSPKNIGKPLGRFVLDIFKFWKPTLSPTNIINDPERSPDFVYTVMATTNLIGVLF
ARSLHYQFLSWYAFSLPYLLYKARLNFIASIIVYAAHEYCWLVFPATEQSSAL
LVSILLILILIFTNEQLFPSQSVPAEKKNT

FIGURE 7 (sheet 1)

P. pastoris ALG3 BLAST

Sequences producing significant alignments:			(bits)	Value
gi 586444 sp P38179 ALG3 YEAST Dolichyl-P-Man:Man(5)GlcNAc(...	228		2e-58	
gi 12802365 gb AAK07848.1 AF309689_10 putative NOT-56 manno...	212		8e-54	
gi 984725 gb AAA75352.1 ORF 1	206		4e-52	
gi 7492702 pir T39084 probable mannosyltransferase - fission	176		8e-43	
gi 16226531 gb AAI16193.1 AF428424_1 At2g47760/F17A22.15 [A...]	164		2e-39	
gi 25367230 pir B84919 Not56-like protein [imported] - Ara...	164		3e-39	
gi 25814791 emb CAB70171.2 Hypothetical protein K09E4.2 [C...]	161		2e-38	
gi 17535001 ref NP_496950.1 Putative plasma membrane membr...	160		3e-38	
gi 1654000 emb CAA70220.1 Not56-like protein [Homo sapiens...]	155		2e-36	
gi 13279206 gb AAH04313.1 AAH04313 Unknown (protein for IMA...)	154		2e-36	
gi 22122365 ref NP_666051.1 hypothetical protein MGC36684 ...	150		3e-35	
gi 21292031 gb EAA04176.1 agCP3388 [Anopheles gambiae str...]	120		4e-26	
gi 1780792 emb CAA71167.1 lethal(2)neighbour of tid [Droso...]	114		3e-24	

Alignments

S. cerevisiae

Score = 228 bits (580), Expect = 2e-58
 Identities = 154/429 (35%), Positives = 229/429 (53%), Gaps = 37/429 (8%)

Query: 9 RPKLTLKNVIGDLVALIQNLFPDFSVFVAPLLWLADSIVIKVIIGTVSYTDIDFSSYM 68
 RP L L DL ++ V+F+ ++ V PLL L +S++ K+II V+YT+ID+ +YM
 Sbjct: 20 RPPLDLWQ---DLKDGVRYVIFDCRANLIVMPPLLILFESMLCKIIIKKVAYTEIDYKAYM 76

Query: 69 QQIFKIR-QGELEDYSNI F GDTGPLVYPAGHVAYSVLSWYSDGGEDVSFVQQAFGWLYLG 127
 +QI I+ G LDYS + G TGPLVYPAGHV Y ++ W ++G + V Q F +LYL
 Sbjct: 77 EQIEMIQLDGMLDYSQVSGGTGPLVYPAGHVLIYKMMYWLTEGMDHVERGQVFFRYLYLL 136

Query: 128 CLLLSISSYFFSGLGKIPPVYFVLLVASKRLHSIFVLRLFNDCLTTFLMLATI---IILQ 184
 L L ++ Y+ L +PP VL SKRLHSI+VLRLFND C TT M+ T+ I+
 Sbjct: 137 TLALQMACYY---LLHLPPWCVVLA CLSKRLHSIYV LRLFND CFTTLMVVTVLGAIVAS 193

Query: 185 QASSWRKDGT TIPLSVPDAADTYSLAISVKMNXXXXXXXXXXXXCDENLIKALAPXX 244
 + K ++ L + + TYS+A+S+KMN D N+I L
 Sbjct: 194 RCHQRPKLKKSLALVI---SATYSMAVS IKMNALLYFPAMMISLFILNDANVIL TLLDV 250

Query: 245 XXXXXXXXXXXXYSFILPLHYDDQANEIRSAYFRQAFDFSRQFLYKWTVNWRFLSQETFNNV 304
 F+ Y AF+F R+F+Y+W++NW+ + +E FN+
 Sbjct: 251 AMIAWQVAVAVPFL-----RSFPQQYLHCAFNFGRKF MYQWSINWQMMDEEA FNDK 301

Query: 305 HFHQLLFALHIITL-VLFILKFLSPKNIGKPLGRFVLDIFKFWKPTLSPTNI IN-DPERS 362
 FH L H+I L LF+ ++ R + D++ L ++N +P ++
 Sbjct: 302 RFHLALLISHLIALTTLFVTRY-----PRILPDLWSSLCHPLRKNAVLNANPAKT 351

Query: 363 PDFVYTVMMATTNLIGVLFARSLHYQFLSWYAFSLPYLLYKARLNFIASIIVYAAHEYCWL 422
 F V+ +N IGVLF+RSLHYQFLSWY ++LP L++ + + F I Y HE+CW
 Sbjct: 352 IPF---VLIASNFIGVLF SRSLHYQFLSWYHWTLPILIFWSGMPFFVGPIWYVLHEWCWN 408

Query: 423 VFPATEQSS 431
 +P Q+S
 Sbjct: 409 SYPPNSQAS 417

FIGURE 7 (sheet 2)

Neurospora crassa

Score = 212 bits (540), Expect = 8e-54
 Identities = 140/400 (35%), Positives = 212/400 (53%), Gaps = 29/400 (7%)

Query: 35 SVFVAPLLWLADSIVIKVIIGTVSYTIDFSSYMQQIFKIRQGELDYSNIFGDTGPLVYP 94
 S + P L+L D+++ +II V YT+ID+++YM+Q+ +I GE DY+ + G GPLVYP
 Sbjct: 33 SKLIPPAFLVLDALLCGLIIWKVPTYEIDWAAYMEQVSQILSGERDYTKVRGGTGPLVYP 92

Query: 95 AGHVHAYSVLSWYSDGGEDVSFVQQAFGWLYLGCLLLSISYYFFSLGKIPPVYFVLLVA 154
 A HV+ Y+ L +D G ++ QQ F LY+ L + + Y+ K PP F LL
 Sbjct: 93 AAHVYIYTGLYHLTDEGRNILLAQQLFAGLYMVTЛАVVMGCYW--QAKAPPYLFPPLLTL 149

Query: 155 SKRLHSIFVLRFNDCLTTFMLATIIILQQASSWRKDGTIPLSVPDAADTYSLAISVK 214
 SKRLHSIFVLR FNDC + I Q+ +W+ A Y+L + VK
 Sbjct: 150 SKRLHSIFVLRCFNDCFAVLFLWLAIFFFQR-RNWQA-----GALLYTLGLGVK 197

Query: 215 MNXXXXXXXXXXXXXXCDENLIKALAPXXXXXXXXXXYSFILPLHYDDQANEIRSAY 274
 M + + L F+ HY + Y
 Sbjct: 198 MTLLLSSLPAVGIVLFLGSG-SFVTTQLVATMGLVQIILIGVPFL--AHYPTE-----Y 247

Query: 275 FRQAFDFSRQFLYKWTVNWRFLSQETFNNVHFHQLLFALHIITLVLFI-LKFLSPKNIGK 333
 +AF+ SRQF +KWTVNWRF+ +E F + F L ALH++ L +FI +++ P K
 Sbjct: 248 LSRAFELSROFFFKWTVNWRFGEEIFLSKGFBTLLALHVLVLGIFITTRWIKPAR--K 305

Query: 334 PLGRFVLDIFKFWKPTLS-PTNIINDPERSPDFVYTVMMATTNLIGVLFARSLHYQFLSWY 392
 L + + KP L+ P + + +P ++ T + + N +G+LFARSLHYQF ++
 Sbjct: 306 SLVQLISPVLLAGKPPLTVPEHRAARDVTPRYIMTTILSANAVGLLFARSLHYQFYAYV 365

Query: 393 AFSLPYLLYKARLNFIASIIVYAAHEYCWLVPATEQSSA 432
 A+S P+LL++A L+ + ++A HE+ W VFP+T SSA
 Sbjct: 366 AWSTPFLLWRAGLHPVLVYLLWAVHEAWNVPSTPASSA 405

Schizosaccharomyces pombe

Score = 176 bits (445), Expect = 8e-43
 Identities = 132/390 (33%), Positives = 194/390 (49%), Gaps = 35/390 (8%)

Query: 42 LWLADSIVIKVIIGTVSYTIDFSSYMQQIFKIRQGELDYSNIFGDTGPLVYPAGHVHAY 101
 L L + + II V YT+ID+ +YM+Q+ GE DY ++ G GPLVYP GHV Y
 Sbjct: 30 LLLLEIPFVFAIISKVPTYEIDWIAYMEQVNSFLGERDYKSLVGCTGPLVYPGGHVFLY 89

Query: 102 SVLSWYSDGGEDVSFVQQAFGWLYLGCLLLSISYYFFSLGKIPPVYFVLLVASKRLHSI 161
 ++L + +DGG ++ Q F ++Y + +I Y F + + P +VLL+ SKRLHSI
 Sbjct: 90 TLLYYLTDGGTNIVRAQYIFAFVYW--ITTAIVGYLFK-IVRAPFYIYVLLILSKRLHSI 146

Query: 162 FVLRFLNDCLTTFLMLATIIILQQASSWRKDGTIPLSVPDAADTYSLAISVKMNXXXX 221
 F+LRLFND + L + I+ W + A+ S+A SVKM+
 Sbjct: 147 FILRLFNDGFNS-LFSSLFILSSCKKKWV-----ASILLSVACSVKMSSLLYV 194

Query: 222 XXXXXXXXXXXXCDENLIKALAPXXXXXXXXXXYSFILPLHYDDQANEIRSAYFRQAFDF 281
 L++ L P + + + +Y+ QAFDF
 Sbjct: 195 PAYLVL-----LLQILGPKKTWMHIFVIIIVQILFSIPF---LAYFWSYWTQAFDF 242

Query: 282 SRQFLYKWTVNWRFLSQETFNNVHFHQLLFALHIITLVLFLIKFLSPKNIGKPLGRFVLD 341
 R F YKWTVNWRF+ + F + F + LH+ LV F K + + P
 Sbjct: 243 GRAFDYKWTVNWRFIPRSIFESTSFSTSILFLHVALLVAFTCKHWNKLSRATP----- 295

Query: 342 IFKFWKPTLSPTNIINDPERSPDFVYTVMMATTNLIGVLFARSLHYQFLSWYAFSLPYLLY 401
 F L+ + +P+F++T +AT+NLIQ+L ARSLHYQF +W+A+ PYL Y

10/500240

FIGURE 7 (sheet 3)

Sbjct: 296 -FAMVNSMLTLKPLPKLQLATPNFIFTALATSNLIGILCARSLHYQFYAWFAWYSPYLCY 354

Query: 402 KARLNFIASIIVYAAHEYCWLVPATEQSS 431
+A I ++ EY W VFP+T+ SS

Sbjct: 355 QASFPAPIVIGLWMLQEYAWNVPSTKLSS 384
Arabidopsis thaliana

Score = 164 bits (415), Expect = 2e-39
Identities = 131/391 (33%), Positives = 194/391 (49%), Gaps = 29/391 (7%)

Query: 42 LWLADSIVIKVIIIGTVSYTDIDFSSYMQQIFKIROQGELDYSNIFGDTGPLVYPAGHVHAY 101
L LAD+I++ +II V YT ID+ +YM Q+ GE DY N+ GDTGPLVYPAG ++ Y

Sbjct: 39 LILADAILVALIIAYVPTYKIDWDAYMSQVSGFLGGERDYGNLKGDTGPLVYPAGFLYVY 98

Query: 102 SVLSWYSDGGEDVSFVQQAFGWLYLGCLLLSISYYFFSGLGKIPPPVYFVLLVASKRLHSI 161
S + + G +V Q FG LY+ L + + Y + + +P LL SKR+HSI

Sbjct: 99 SAVQNLTGG--EVYPAQILFGVLYIVNLGIVLIIYVKTDV--VPWWALSLLCLSKRIHSI 154

Query: 162 FVLRLFNDCLTTFLMLATIIILQQASSWRKDGTIPLSVPDAADTYSLAISVKMNXXXXX 221
FVLRLFNDC L+ A++ + +RK + + +S A+SVKMN

Sbjct: 155 FVLRLFNDCFAMTLLHASMALFL---YRKWHLGMLV-----FSGAVSVKMNVLLYA 202

Query: 222 XXXXXXXXXXXCDENLIKALAPXXXXXXXXXXYSFILPLHYDDQANEIRSAYFRQAFDF 281
N+I ++ F++ +Y AFD

Sbjct: 203 PTLLLLLKKAM--NIIGVV SALAGAALA QILVGLPFLITYPV-----SYIANAFDL 251

Query: 282 SRQFLYKWTVNWRFLSQETFNNVHFHQLLFALHIITLVLFILKFLSPKNIGKPLGRFVLD 341
R F++ W+VN++F+ + F + F L H+ LV F + K+ G +G

Sbjct: 252 GRVFIHFWSVNFKFVPERVFSKEFAVCLLIAHLPILLVAFA-NYKWCKHEGGIIGFMRSR 310

Query: 342 IFKFWKP-TLSPTNIINDPERSPDFVYTVMATTNLIGVLFARSLHYQFLSWYAFSLPYLL 400
F P +LS +++ + + V T M N IG++FARSLHYQF SWY +SLPYLL

Sbjct: 311 HFFLTLPSLSSFSDVSASRIITKEHVVTAMFVGFIGIVFARSLHYQFYSWYFSLPYLL 370

Query: 401 YKARLNFIASIIVYAAHEYCWLVPATEQSS 431
++ +I++ E CW V+P+T SS

Sbjct: 371 WRTPFPTWLRLIMFLGIELCWNVYPSTPSSS 401

10/500240

FIGURE 8

K. lactis ALG3

TTTGTTCACAAGCTGATACCAACGAACATGAATAACCCGGCAGGTTACT
GAAGATTGGCAAAGCTAACCTTTACATCCTTACCGATGCTGTATTCAG
TGCATGAGAGTAAACGCAGAACAAATTGCATACATTTACTTGTACCA
ATTACATTGGAGTACTATTGCTCGATCATTACACTACCAATT CCTATCTT
GGTACCATTGGACGTTACCAAGTACTATTGAATTGGGCCAATGTTCCGTATC
CGCTATGTGTGCTATGGTACCTAACACATGAGTGGTGCTGGAACAGCTAT
CCGCCAAACGCTACTGCATCCACACTGCTACACGCGTGTAAACACATACTG
TTATTGGCTGTATTCTTAAGAGGACCCGCAAACACTCGAAAAGTGGTGATAA
CGAAACAAACACACGAGAAAGCTGAG

K. lactis Alg3p

FVYKLIPTNMNTPAGLLKIGKANLLHPFTDAVFSAMRVNAEQIAYILLVTNYI
GVLFARSLHYQFLSWYHWTLPVLLNWANVPYPLCVLWYLTHEWCWNSYPP
NATASTLLHACNTCYWLYSZEDPQTRKVITKQHTRKL

10/500240

FIGURE 9

K. lactis ALG3 BLAST

Score	E		
Sequences producing significant alignments:		(bits)	Value
gi 586444 sp P38179 ALG3 YEAST	Dolichyl-P-Man:Man(5)GlcNAc(...	125	1e-28
gi 984725 gb AAA75352.1	ORF 1	94	4e-19
gi 16226531 gb AAL16193.1 AF428424_1	At2g47760/F17A22.15 [A...	72	1e-12
gi 25367230 pir B84919	Not56-like protein [imported] - Ara...	72	1e-12
gi 21292031 gb EAA04176.1	agCP3388 [Anopheles gambiae str....	69	2e-11
gi 20892051 ref XP_148657.1	similar to Lethal(2)neighbour ...	65	2e-10

Alignments

S. cerevisiae

Score = 125 bits (314), Expect = 1e-28
Identities = 60/120 (50%), Positives = 83/120 (69%), Gaps = 1/120 (0%)
Frame = +3

Query: 66 ANLLHPFT-DAVFSAMRVNAEQIAYILLVTNYIGVLFARSLHYQFLSWYHWTLPVLLNWA 242
++L HP +AV +A A+ I ++L+ +N+IGVLF+RSLHYQFLSWYHWTLP+L+ W+
Sbjct: 332 SSLCHPLRKNAVLNANP--AKTIPFVLIASNFIGVLFSRSLHYQFLSWYHWTLPILIFWS 389

Query: 243 NVPYPLCVLWYLTHEWCWNNSYPPNATASTLLHACNTCYWLYS*EDPQTRKVVITKQHTR 422
+P+ + +WY+ HEWCWNNSYPPN+ ASTLL A NT L + + V + K H R
Sbjct: 390 GMPFFVGPIWYVLHEWCWNNSYPPNSQASTLLLALNTVLLLLA-LTQLSGSVALAKSHLR 448

A. thaliana

Score = 72.0 bits (175), Expect = 1e-12
Identities = 42/107 (39%), Positives = 57/107 (53%), Gaps = 3/107 (2%)
Frame = +3

Query: 84 FTDAVFSAMRVNAEQIAYILLVTNYIGVLFARSLHYQFLSWYHWTLPVLLNWANVPYPLC 263
F+D S + + E + + V N+IG++FARSLHYQF SWY ++LP LL P L
Sbjct: 322 FSDVSASRI-ITKEHVVTAMFVGFIGIVFARSLHYQFYSLPYLLWRTPFTWL 380

Query: 264 VLWYLTHEWCWNNSYPPNATASTL---LHACNTCYWLYS*EDPQTRK 395
++ +L E CWN YP + +S L LH WL DP K
Sbjct: 381 LIMFLGIELCWNVYPSTPSSGLLCLHLIIIVGLWLAPSVDPYQLK 427

10/500240

FIGURE 10

S. cerevisiae ALG9

ATGAATTGCAAGCGGTAAACCATTAGTTATTACTGTTGTTATTTTAACAAGAGT
ATATATTCAAGCCGACATTCTCGTTAATTTCAGATTGCGATGAAACTTTAATTATT
GGGAACCATTAAATTATTGGTACGTGGATTGGTAAACAAACCTGGGAATATT
ACCCGAGTATTCTATTAGATCATGGCTTCTTATTACCTTTACTGTATTCTTA
TCCAGTAAACAAATTACTGACCTAGAAAGTCATTGGAACCTTTCATCACAAGA
GCATGCTTAGGCTTTAGTTATCATGGAATTAAACTACATCGTGAATTGC
AGGCAGCTTGGCATTGCAAATCGAAATATTGGATTATTCCAATTGTTAAC
CGGGCTGGTTCCATGCATCTGTGGAATTATTGCCCTCTGCCGTTGCCATGTTG
TATGTAGGTGCCACCAGACACTCTACGCTATCTGTCCACTGGGTCTACTTCTAA
CTTACGAAAAGTTAGCGTACAATTCTGGCTAGTATACTAGGCTGGCCATTG
TTTAATTAAAGCTTGCCTATTGTTACATTACCTTTCAACCATAAGAATTATT
CTACCATCAGAACCGCATTGACTGCTGTTGATATTCAATTGACTGCATTGCT
GTGATTGTCAGTACAGTATATTACGGGAAGCTGCTCTGTATCATGGAACA
TCTTATTAAACAATGTCATTAATGCAAGTGAGGAATCTGCCAAATATTGCGG
GTTGAGCCATGGTACTACTATCCACTAAATTGTTACTGAATTCCCAGTGCCTGT
GCTAGTTTAGCTATTGGAAATTCCATTGAGATTGCCATTATGGGCAT
CATTATTACATGGATTGCCGTTCACTCAACAAACCTCACAAAGAGGAAAGATT
TCTCTATCCAATTACGGGTTAATAACTTGAGTGCAAGTATGCCCTTACAAAG
TGTGAAATCTATTCAATAGAAAGCCATTCTAAAAAGGTATAAAGTTGTCAGT
TTTATTAAATTGTCAGGCCAGGCAATGTCACGGGATAGTGGCTTGGTACA
TACACAGCTCTATAGCCGTACGAGCAATTCTTCACTAAATCAAGGGTG
TGAAGGCACCGGTAGTGAATGTATGTACGGGACGTGAATGGTACTTCCAAG
TTCTTCTGCTGCCAGATAATCATAGGCTAAAATTGTTAAATCTGGATTGATG
GTCTTCTCCAGGTGATTCCAGAGAGTGGTCTATTCAAAAAGATTAGAACT
TTACCTAAGGGAAATGAATAACAAGAATATATGATACCGGTAAGAGTGGCG
ATCACTAGATGTGATTATTGACATCGTCGCCAAATAATTAAACAAAG
ACGTTTCACCCCTCATCTGATGGATAACTGGAATAAGCTGGCATGTGCTGC
ATTCAATCGACGGTAAAATTCTAAGATTGGTAGAGCATTACGTACCGGAG
CCAATCAACCGAATCATGCAAATAGTTACCAAAACAATGGAATCAAGTGTACG
GTGTTCGTTACATTGATTACTGTTGTTGAAAAACCAACTGAGACTACTAATTGA

S. cerevisiae Alg9p

MNCKAVTISLLLLLFLTRVYIQPTFSLISDCDETNYWEPLNLLVRGFGKQTWEYSPE
YSIRSWAFLPFYCILYPVNKFDTLESHWNFFITRACLGFFSFIMEFKLHREIAGSLALQ
IANIWIIFQLFNPGWFHASVELLPSAVAMLLYVGATRHSRLYSTGSTSNFTKSLAYN
FLASILGPFWVLISLPLCLHYLFNHRISTIRTAFDCCCLIFSLTAFAVIVTDSIFYGKLAP
VSWNILFYNVINASEESGPNIIGVEPWYYPLNLLNFPLPVLVLAIGIFHLRLWPLW
ASLFTWIAVFTQQPHKEERFLYPIYGLITSASIAFYKVNLNRKPILKKGIKLSVLLI
VAGQAMSRIVALVNNTAPIAVYEQFSSLNQGGVKAPVVNVCTGREWYHFPSFLLP
DNHRLKFVKSGFDGLLPDFPESGSIFKKIRTLPKGMNNKNIYDTGKEWPITRCDYFI
DIVAPINLTKDVFNPPLHLMNDWNKLACAAFIDGENSKILGRAFYVPEPINRIMQIVLP
KQWNQVYGVRYIDYCLFEKPTETTN

A. 9 17

FIGURE 11

P. pastoris ALG9

TGGCCTCCTGCTCGATACTTCCTTTACAGTAACCAACATACATGTT
CTCCAACATGCTCTGTATGTATTGGCCTATTCTATCTTGAGACTTGATATC
AACCTCTATGGTATTATTCAGACTGTGATGAAGTGTCAACTACTGGGA
GCCACTCAACTCATGCTTAGAGGGTTGGAAAACAGACTTGGGAGTATT
CTCCAGAGTATGCCATCCGATCTGGTCTATCTAGTGCCACTTGGATAG
CAGGCTATCCACCATTGTTCTGGATATCCCTCTTACTACTTTCTACTT
TTTCAGACTACTGCTGGTTATTTTCATTGGTGCAGAAGTCAAGTTGTA
CCATAGTTGAAGAAAAATGTCAGCAGTAAGATCAGTTCTGGTACCTTCT
ATTTACAACCGTTGCTCCAGGAATGTCATAGCACGATAGCCTTATTACC
ATCCTCTTGCTATGGTTGTCACACTTTGCCATTAGATACGTCAATTGAT
TACCTACAATTACCAACATTAATGCGCACAATCAGAGAGACTGCTGCCAT
CTCACCAAGCTCACAAACAACACTAGCCAACCTCTCTC

P. pastoris Alg9p

WPSCLLDTSFYSNQHTCSPTCSCMYWPILSZDLISTFYGIISDCDEVFNYWEPL
NFMLRGFGKQTWEYSPEYAIRSWSYLVPLWIAGYPPLFLDIPSYYFFYFFRLLL
VIFSLVAEVKLYHSLKKNVSSKISFWYLLFTTVAPGMSHSTIALLPSSFAMVCH
TFAIRYVIDYLQLPTLMRTIREAAISPAAHKQQLANSL

FIGURE 12 (sheet 1)*P. pastoris* ALG9 BLAST

Score E
 Sequences producing significant alignments: (bits) Value

gi 6324110 ref NP_014180.1	catalyzes the transfer of manno...	131	1e-29
gi 21296668 gb EAA08813.1	agCP7810 [Anopheles gambiae str...	110	2e-23
gi 7019765 emb CAB75773.1	putative mannosyltransferase inv...	104	1e-21
gi 26341066 dbj BAC34195.1	unnamed protein product [Mus mu...	99	4e-20
gi 16551378 gb AAL25798.1	DIBD1 [Homo sapiens]	99	4e-20
gi 19527202 ref NP_598742.1	RIKEN cDNA 8230402H15 [Mus mus...	99	4e-20
gi 12053349 emb CAB66861.1	hypothetical protein [Homo sapi...	99	4e-20

Alignments

S. cerevisiae

Score = 131 bits (329), Expect = 1e-29
 Identities = 62/141 (43%), Positives = 91/141 (64%), Gaps = 1/141 (0%)
 Frame = +2

Query: 200 ISTFYGIISDCDEVFNYWEPLNFMLRGFGKQTWEYSPEYAIRSWSYLVPLWIAGYP-PLF 376
 I + +ISDCDE FNYWEPLN ++RGFGKQTWEYSPEY+IRSW++L+P + YP F
 Sbjct: 21 IQPTFSLISDCDETFNYWEPLNLLVRGFGKQTWEYSPEYSIRSWAFLPFYCILYPVNKF 80

Query: 377 LDIPSXXXXXXXXXRLLVIFSLVAEVKLYHSLKKNVSSKISFWYLLFTTVAPGMSHSTIAL 556
 D+ S R L FS + E KL+ + +++ +I+ +++F PG H+++ L
 Sbjct: 81 TDLESHWNFFITRACLGFPSIMEFKLHREIAGSLALQIANIWIIFQLFNPGWFHASVEL 140

Query: 557 LPSSFAMVCHTFAIRYVIDYL 619
 LPS+ AM+ + A R+ + YL
 Sbjct: 141 LPSAVAMLLYVGATRHSLRYL 161

Anopheles gambiae

Score = 110 bits (274), Expect = 2e-23
 Identities = 58/130 (44%), Positives = 79/130 (60%), Gaps = 3/130 (2%)
 Frame = +2

Query: 197 LISTFYGIISDCDEVFNYWEPLNFMLRGFGKQTWEYSPEYAIRSWSYLVPLWIAGYPPLF 376
 L S Y IIISDCDE +NYWEPL+++L+G G QTWEYSPE+A+RS+SY LW+ G P
 Sbjct: 34 LQSALYSIISDCDETYNYWEPLHYLLKGKGQTWEYSPEFALARSYSY--LWLHGLPAKV 90

Query: 377 LDIPS---XXXXXXXXXRLLVIFSLVAEVKLYHSLKKNVSSKISFWYLLFTTVAPGMSHST 547
 L + + R LL + + E +LY L + + + LLF + GM S+
 Sbjct: 91 LQLMTDNGVLIFYFVRCLLAVTALLEYRLYRILGRKCGGGVASLWLLFQLTSAGMFISS 150

Query: 548 IALLPSSFAM 577
 ALLPSSF+M
 Sbjct: 151 AALLPSSFSM 160

10/500240

FIGURE 12 (sheet 2)

S. pombe

Score = 104 bits (260), Expect = 1e-21
Identities = 58/157 (36%), Positives = 85/157 (54%)
Frame = +2

Query: 197 LISTFYGIISDCDEVFNYWEPLNFMRLRGFGKQTWEYSPEYAIRWSYLVPLWIAGYPPFLF 376
L S + +I DCDEV+NYWEPL+++L G+G QTWEYSPEYAIRSW Y+ + G+
Sbjct: 26 LTSASFRVIDDCDEVVNYWEPLHYLLGYGLQTWEYSPEYAIRSWFYIALHAVPGFLARG 85

Query: 377 LDIPSXXXXXXXXRLLLVI FSLVAEVKLYHSLKKNVSSKISFWYLLFTTVAPGMSHSTIAL 556
L + R +L FS E L ++ +N + ++ V GM ++ +
Sbjct: 86 LG LSR LHVFY FIRGV LACFS AF C ETNL L I L A V AR N FN R A V AL H LT SV LFVN SGM WS A ST SF 145

Query: 557 LPSSFAMVCHTF AIRY VIDYLQLPTLMRTIREAAIS 667
LPSSFAM T A+ L P+ RT++ + I+
Sbjct: 146 LPSSFAMNMVTLALS---AQLSPPSTKRTVKVVSFIT 179

M. musculus

Score = 99.4 bits (246), Expect = 4e-20
Identities = 57/143 (39%), Positives = 76/143 (53%), Gaps = 1/143 (0%)
Frame = +2

Query: 152 SPTCSCMYWPILS*DLISTFYGIISDCDEVFNYWEPLNFMRLRGFGKQTWEYSPEYAIRSW 331
+P S + +LS L + ISDCDE FNYWEP ++++ G G QTWEYSP YAIRS+
Sbjct: 55 APEGSTAFKCLLSARLC ALLSNISDCDET FNYWEPTHYLIYGKGFQTWEYSPVYAIRSY 114

Query: 332 SY-LVPLWIAGYPPFLDIPSXXXXXXXXRLLLVI FSLVAEVKLYHSLKKNVSSKISFWYL 508
+Y L+ W A + L R LL S V E+ Y ++ K +S L
Sbjct: 115 AYLLLHAWPAAFHARILQTNKILVFYFLRCLLA FVSCV CELYFYKAVCKKFGLHVSRMML 174

Query: 509 LFTTVAPGM SHSTIA LL PSSF AM 577
F ++ GM S+ A LPSSF M
Sbjct: 175 AFLVLSTGMFCSSSAFLPSSFCM 197

H. sapiens

Score = 99.4 bits (246), Expect = 4e-20
Identities = 56/143 (39%), Positives = 76/143 (53%), Gaps = 1/143 (0%)
Frame = +2

Query: 152 SPTCSCMYWPILS*DLISTFYGIISDCDEVFNYWEPLNFMRLRGFGKQTWEYSPEYAIRSW 331
+P S + +LS L + ISDCDE FNYWEP ++++ G G QTWEYSP YAIRS+
Sbjct: 55 APEGSTAFKCLLSARLC ALLSNISDCDET FNYWEPTHYLIYGEGFQTWEYSPAYAIRSY 114

Query: 332 SY-LVPLWIAGYPPFLDIPSXXXXXXXXRLLLVI FSLVAEVKLYHSLKKNVSSKISFWYL 508
+Y L+ W A + L R LL S + E+ Y ++ K +S L
Sbjct: 115 AYLLLHAWPAAFHARILQTNKILVFYFLRCLLA FVSCV CICELYFYKAVCKKFGLHVSRMML 174

Query: 509 LFTTVAPGM SHSTIA LL PSSF AM 577
F ++ GM S+ A LPSSF M
Sbjct: 175 AFLVLSTGMFCSSSAFLPSSFCM 197

FIGURE 13

S. cerevisiae ALG12

ATGCCTGGTCTGCCCTGATAACAGTGTATTGACCGTGATTCCTTCATCTAAT
 CCAAGCTCATTACCAAGGTGGAAGAGAGTTTAATATTCAAGCCATTGATGAT
 ATTTAACCTACAGCGTATTGATATCTCCAATATGACCACTGAAATTCTGG
 AGTAGTCCCTAGAACATTGCTGGTGTGATTATTGCAATGCTTCGAGACCTT
 ATCTTACTTGAGTCTTGATCCAAACTCCAGGCCTACGTCTATAGATGTTCAA
 TTGGTCTAGGGGGATTGTTGGCCTACCAATGGGTTCTTATCTATTAAA
 GAATTGTTGCAAGATATGTTGATGAAATCACTGAAAAGAAAAAGGAAGAAAA
 TGAAGACAAGGATATACATTACGATAGCGCTGGTACATGGTTCTTATT
 TAATTGGCAGTTCCACCTCATGTTCTACAGCACTAGGACTCTGCCTAATTGTC
 ATGACTCTGCCTCAACCAACGTCGATTGGGTTGGTTATGGTCTGTTATAA
 TGCAGCTATATTCTATCTGCGCTCGTGGCAATTGTTAGACTGGAAGTGTCA
 CTCTCAGTGCTGGTATTGCTCTATTAGCGTCATCTCAAGAAGATTCTTATT
 GATGCTATCAAATTGGTATCTTGCTGGACTTGGTCCGCCATCAGTATCAC
 CGTTGATTCAATTCTGGCAAGAATGGTGTCTACCTGAGGTAGATGGTTCTTGT
 TCAACGTGGTGCAGGTTACGCTTCCAAGTGGGTGTGGAGCCAGTTACTGCTTA
 TTTACGCATTACTGAGAATGATGTTATGCCACCAACTGTTTACTATTGAATT
 ACTTCGGCTATAAATTAGCACCTGCAAAATTAAAAATTGCTCTACTAGCATCTCTT
 TTCCACATTATCGTCTTATCCTTCAACCTCACAAAGAATGGAGATTCACTATCTA
 CGCTGTTCCATCTATCATGTTGCTAGGTGCCACAGGAGCAGCACATCTATGGGAG
 AATATGAAAGTAAAAAGATTACCAATGTTTATGTTGGCTATATTGCCCTTATC
 TATAATGACCTCCTTTTCAATTCAATGGCCTTGTATATATCAAGAATGAATT
 ATCCAGGCGGGAGGCTTAACCTCTTAAATGACATGATTGTGGAAAAAAATAT
 TACAAACGCTACAGTCATATCAGCATACCTCTTGATGACAGGTGTCACTTTAT
 TTGGTGAATTGAACTACGGTGTACGGCATCAATTACGATAAGACTGAAATAC
 GACTTACTGCAGGAATGTGGCCCTCTTGTATTCTGATCACCCACGAGCCA
 ACCGCCTCTCAATTGCCATTGAGAATAAGACTACCAACCATTGGAGCTAGTTA
 ACACAAACAAAGATGTTACTGGATTGACCCAAACCTACATTAAAGAACTTGT
 CCAAGAGAGAGTGAATGTTGTCTACTCAAACAGATCATTGACAAAGACC
 CCTACCGTTTTGAAAGAATTGACGCCAATTGATGTTAAAAGCGATGTCTT
 CTTCACCTATAAGAGAATCAAACAAGATGAAAAACTGATTGA

S. cerevisiae Alg12p

MRWSVLDTVLLTVISFHILQAPFTKVEESFNIQAIHDILTYSVFDISQYDHLKFPGVVP
 RTFGAVIILMLSRPYLYLSSLIQTSRPTSIVQLVVRGIVGLTNGLSFIYLKNCLQDM
 FDEITEKKKEENEDKDIYIYDSAGTWFLFLIGSFHLMFYSTRTPNFMVTLPLTNVAL
 GWVLLGRYNAAIIFSLALVAIVFRLEVSAALSAGIALFSVIFKKISLFDAIKFGIFGLGLGS
 AISITVDSYFWQEWCPLPEVDGFLFNVVAHYASKWGVEPVAYFTHYLRRMMFPPTV
 LLLNYFGYKLAPAKLKIVSLASFHIIVLSPQPHKEWRFIYAVPSIMLLGATGAHLW
 ENMKVKKITNVLCLAILPLSIMTSFFISMAFLYISRMNYPGGEALTSFNDMIVEKNITN
 ATVHISIPPCMTGVTLFELNYGVYGINYDKTENTTLLQEMWPSFDLITHEPTASQLP
 FENKTTNHWELVNTTKMFTGFDPYIKNFVFQERVNVLSSLKQIIFDKTPTVFLKELT
 ANSIVKSDVFFTYKRIKQDEKTD

10/500240

FIGURE 14

P. pastoris ALG12

TCGGTCGAGAATGATAACTGAAGAACTCAAAATCTCTCACACTTCATCGT
TACTGTACTGGCAATCATTGCATTGCAGCCTCATAAAGAAATGGAGATTAT
AGTTTACATTGTTCCACCACTTGTATCACCATACTACAGTACTTGCACA
ACTACCCAGGAGATTACAATCGTCAAAGTTGCTGTTTCTCTAAAGTT
CGGCTCTTGCTCATATCCCTGCGTTCTTCATCTCATCGTATAACTAC
CCTGGGGGTGAAGCTTACAGCATTGAACGAGAAACTCCTTACTGGA
CCAAAGTTCCCTACCTGTTGATATTAAGGTTCATATGGATGTCCTGCATG
CATGACTGGGGTGAATTGTTACTGGATAACTCAAAATTGAACAA
TTAAGAATTGTCTATGATAAAACAGAACAGACGAGTCGCTGGACACAATCT
GGGATTCTTCATTATGTATCTCCGAAATTGACTTGGATTCTCGACTG
CTCCCAAATGGGAGGGGGATTGGCTGAAGATTGATGTTGTCAGGCTAC
AACGGCATCAATAAACAACTATCAAAATACAATTTCATTATGGAAT
ACTTAAACGGATGATAAGAGACGCAACCAACTTGTGATGTTGATTATTC
GTACGGTCTTCGATCCTCATAAAATTGATGATAAAATTATTCAATTATG
AGAGGAGCAGTCAAACCTGAAAATATACCTCATTGTTCAATTGGTGT
AAAGAGTGTGGCGGATAGACTTCTGTAAATCAGGAAAGCTACAATTCCA
ATTGCTGCAAAAATACCAATGCCATAA

P. pastoris Alg12p

RMITEELKISHTFIVTVLAIIFQPHKEWRFIVYIVPPLVITISTVLAQLPRRFTIV
KVAVFLLSGSLLISLSFLFISSYNYPGGEALQHLNEKLLLLDQSSLVDIKVH
MDVPACMTGVTLFGYLDNSKLNNLRIVYDKTEDESLDTIWDSFNYVISEIDL
SSTAPKWEGDWLKIDVVQGYNGINKQSICKNTIFNYGILKRMIRDATKLDVGFI
RTVFRSFIFDDKLFIYERSSQ

10/500240

FIGURE 15 (sheet 1)

P. pastoris ALG12 BLAST

Sequences producing significant alignments:	Score (bits)	E Value
gi 1302525 emb CAA96310.1 ORF YNR030w [Saccharomyces cerev...	102	5e-21
gi 19112221 ref NP_595429.1 putative involvement in cell w...	56	5e-07
gi 15864569 emb CAC83681.1 putative dolichyl-p-man: Man7Glc...	53	4e-06
gi 13129114 ref NP_077010.1 dolichyl-p-mannose:Man7GlcNAc2...	53	4e-06
gi 22266724 gb AAM94900.1 AF311904_1 membrane protein SB87 ...	53	4e-06
gi 18478284 emb CAD22101.1 putative mannosyltransferase [M...	52	8e-06

Alignments

S. cerevisiae

Score = 102 bits (255), Expect = 5e-21
Identities = 74/258 (28%), Positives = 121/258 (46%), Gaps = 19/258 (7%)

Query: 8 RMITEELKISHTFIVTVLAIIAFQPHKEWRFIVYIVPPLVITISTVLAQLP... 187
++ + LKI + + + +++FQPHKEWRFI+Y VP + + + T A L + K+
Sbjct: 302 KLA PAKLKIVSLASLFHIIVLSFQPHKEWRFIIYAVPSIMLLGATGA... 361

Query: 188 -----VXXXXXXXXXXXXXXXXXXXXYYPGGEALQHLNEKLLL... 346
+ NYPPGGEAL N+ ++ + VH+
Sbjct: 362 NVLCLAILPLSIMTSFFFISMALFLYISRNMYPGGEALTSFNDMIV---EKNITNATVHIS 417

Query: 347 VPACMTGVTLFGYLDNSKLNNLRIVYDKTEDES-LDTIWDSFNYVI-----SEIDL... 505
+P CMTGVTLFG L+ I YDKTE+ + L +W SF+++I S++ ++
Sbjct: 418 IPPCMTGVTLFGELNYGVYG---INYDKTENTTLLQEMWPSFDLITHEPTASQLPFENK 474

Query: 506 TAPKWEGDWLKIDVVQGYNGINKQSIKNTIFN-----Y... 670
T WE ++ + + G + IKN +F +LK++I D K F++ +
Sbjct: 475 TTNHWE---LVNTTKMFTGFDPTYIKNFVFQERVNVL... 528

Query: 671 RSFIFDDKLFIFYERSSQ 724
+ I D F Y+R Q
Sbjct: 529 ANSIVKSDVFFTYKRIKQ 546

S. pombe

Score = 56.2 bits (134), Expect = 5e-07
Identities = 46/152 (30%), Positives = 62/152 (40%), Gaps = 11/152 (7%)

Query: 65 II AFQPHKEWRFIVYIVPPLVITISTVLAQL-----PRRFTIVKVAVXXXXXX 220
+ + F HKEWRFI+Y + P S + A L + F I+++
Sbjct: 295 VYSFLIGHKEWRFIIY... -PWFNAASAIGASLCFNASKFGKKIFEILRLMFSGIIFGF... 353

Query: 221 XXXXXXXX...YYPGG AL L E + VHMDV CMTG+T F L +
Sbjct: 354 SSFLLYVFQYAYPGGLALTRLYE-----IENHPQVS... 404

10/500240

FIGURE 15 (sheet 2)

Query: 401 LNNLRIVYDKTEDESL---DTIWDSFNYVISE 487
YDKTED + F+Y+I+E
Sbjct: 405 ----WYYDKTEDPKMLSNSLFISQFDYLITE 431

Homo sapiens

Score = 53.1 bits (126), Expect = 4e-06
Identities = 41/149 (27%), Positives = 68/149 (45%), Gaps = 6/149 (4%)

Query: 59 LAIIAFQPHKEWRFIVYIVPPLVITISTVLAQLPRR-----FTIVKVAVXXXXXXXXXX 220
+A+ + PHKE RFI+Y P L IT + + L + + V
Sbjct: 299 MALYSLLPHKELRFIIYAFPMLNITAARGCSYLLNNYKKSWLYKAGSLLVIGHLVNAAY 358

Query: 221 XXXXXXXXXNYPGGGEALQHLNEKLLLLDQSSLPVDIKVHMDVPACMTGVTLFGYLDNSK 400
+NYPGG A+Q L++ L+ Q+ D+ +H+DV A TGV+ F +++++
Sbjct: 359 SATALYVSHFNYPGGVAMQRLHQ--LVPPQT----DVLLHIDVAAAQTGVSRLQVNSAW 412

Query: 401 LNNLRIVYDKTEDESLDTIWDSEFNYVISE 487
YDK ED T ++ +++ E
Sbjct: 413 R-----YDKREDVQPGTGMLAYTHILME 435

Applied Biosystems Voyager System 6235

Voyager Spec #1 [BP = 1463.3, 2852]

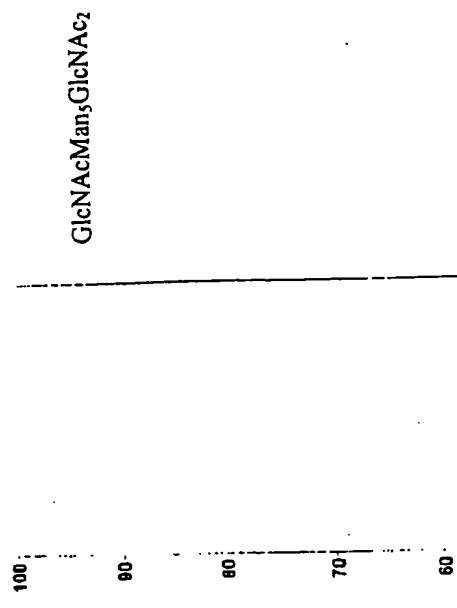


FIGURE 16

10 / 500240

Mode of operation:	Linear
Extraction mode:	Delayed
Polarity:	Positive
Manual	
2852.0 Acquisition control:	
Accelerating voltage:	20000 V
Grid voltage:	93%
Guide wire 0:	0.1%
Extraction delay time:	125 nsec
Acquisition mass range: 850 -- 3200 Da	
Number of laser shots:	200 spectrum
Laser intensity:	2788
Laser Rep Rate:	20.0 Hz
Calibration type:	Default
Calibration matrix:	a-Cyano-4-hydroxydinitro ac
Low mass gate:	800 Da
Digitizer start time:	19.955
Bin size:	0.5 nsec
Number of data points:	37310
Vertical scale:	500 mV
Vertical offset:	0%
Input bandwidth:	500 MHz
Sample wait:	22
Plate ID:	100 WELL PLATE
Serial number:	6235
Instrument name:	Voyager-DE PRO
Plate type filename:	C:\VOYAGER\100_well_plate.p1
Lab name:	PE Biosystems
Absolute X-position:	6212.96
Absolute Y-position:	35933.8
Relative X-position:	-454.524
Relative Y-position:	-1213.7
Shots in spectrum:	200
Source pressure:	6.93e-007
Mirror pressure:	8.615e-008
TC2 pressure:	0.01188
TIS gate width:	10
TIS flight length:	888

Printed: 10:47, December 18, 200

Acquired: 11:42:00, November 08, 2002
Instrument: Voyager-DE PRO
Software: Voyager-DE PRO
Data File: C:\VOYAGER\100_well_plate.p1

Applied Biosystems Voyager System 6235

Voyager Spec #1[BP = 1259.4, 5924]

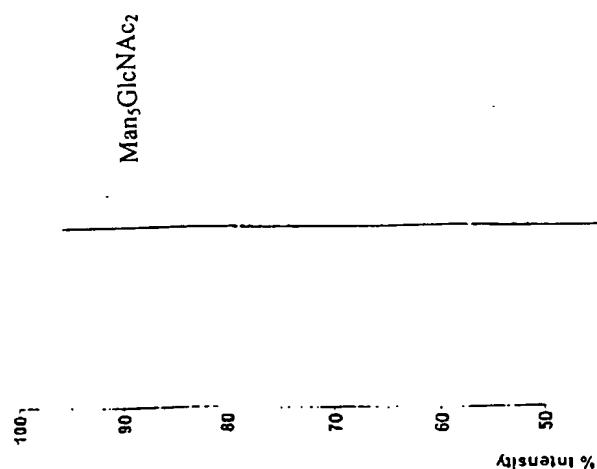


FIGURE 17

Mode of operation:	Linear
Extraction mode:	Delayed
Polarity:	Positive
Acquisition control:	Manual
S924.0	
Accelerating voltage:	20000 V
Grid voltage:	93%
Guide wire 0:	0.1%
Extraction delay time:	125 nsec
Acquisition mass range:	850 -- 3200 Da
Number of laser shots:	200/specum
Laser intensity:	2886
Laser Rep Rate:	20.0 Hz
Calibration type:	Default
Calibration matrix:	a-Cyano-4-hydroxychromanic acid
Low mass gate:	800 Da
Digitizer start time:	19.955
Bin size:	0.5 nsec
Number of data points:	37310
Vertical Scale:	500 mV
Vertical offset:	0%
Input bandwidth:	500 MHz
Sample well:	32
Plate ID:	100 WELL PLATE
Serial number:	6235
Instrument name:	Voyager-DE PRO
Plate type filename:	C:\VOYAGER\100_well_plate.p
Lab Name:	PE Biosystems
Absolute x position:	6613.36
Absolute y position:	30906.1
Relative x position:	-54.1439
Relative y position:	-1261.39
Shots in specum:	200
Source pressure:	7.709e-007
Mirror pressure:	9.387e-008
TC2 pressure:	0.01262
TIS gate width:	10
TIS flight length:	669

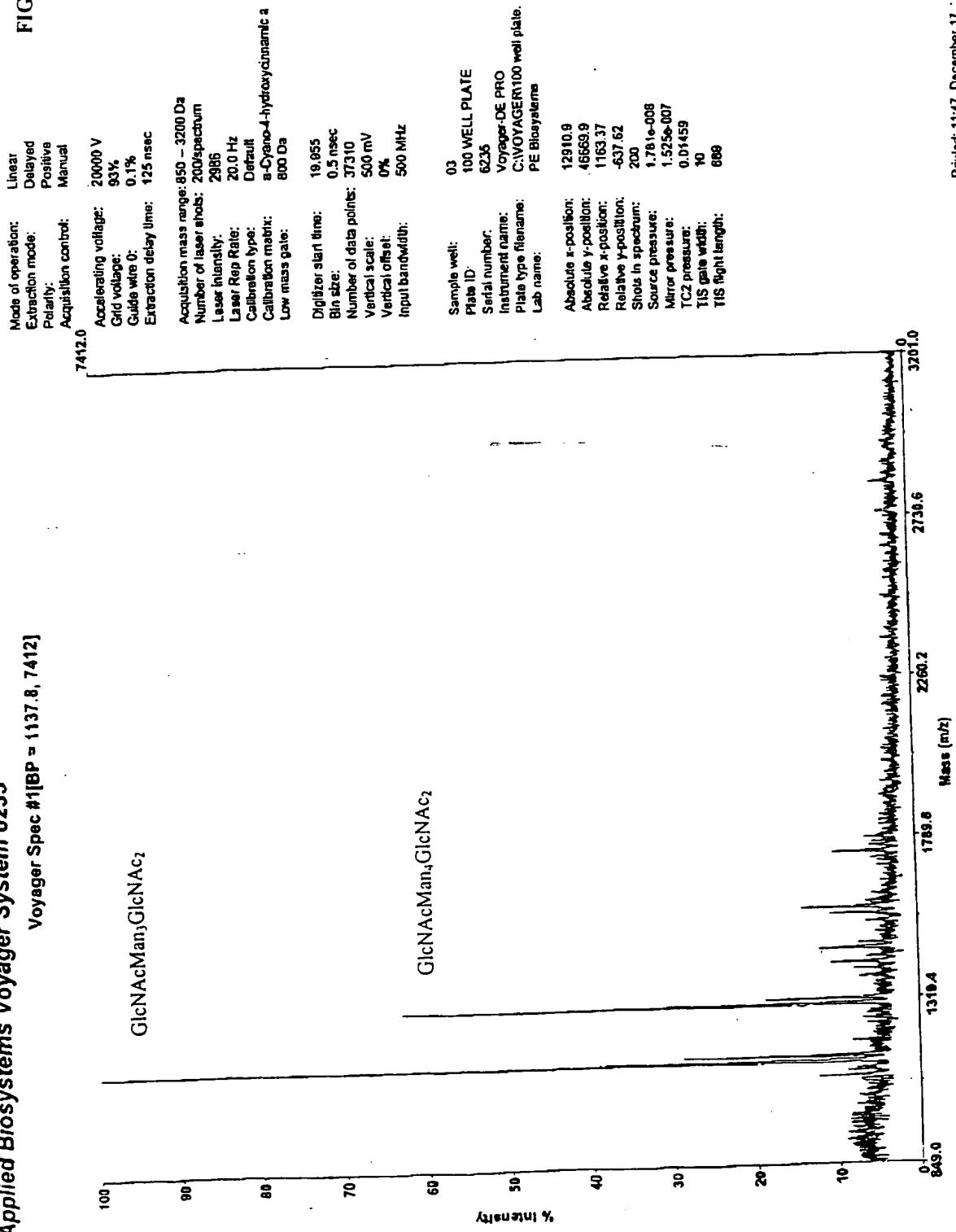
Acquired: 11:30:00, November 08, 2002
Printed: 10:47, December 18, 2002
for him/her (or me) at 11.5.27 PM 11/21/02 by 10.21.02 have all rights reserved.

Printed: 10:47, December 18, 2002

10 / 500240

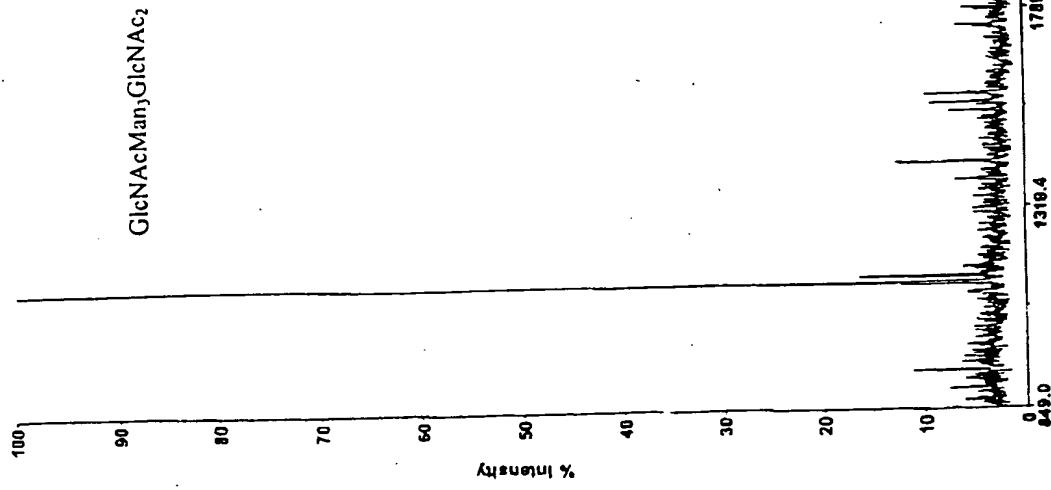
Applied Biosystems Voyager System II Data
Voyager Spec #1[BPP = 1137.8, 7412]

FIGURE 18



Applied Biosystems Voyager System 6235
Voyager Spec #1[BP = 1139.5, 4716]

FIGURE 19



Mode of operation:	Linear
Extraction mode:	Delayed
Polarity:	Positive
Acquisition control:	Manual
4716.0	
Accelerating voltage:	20000 V
Grid voltage:	93%
Guide wire 0:	0.1%
Extraction delay line:	125 nsec
Acquisition mass range: 850 - 32000 Da	
Number of laser shots:	2004 spectrum
Laser Intensity:	2786
Laser Rep Rate:	20.0 Hz
Calibration type:	Default
Calibration matrix:	α -Cyanohydroxydynamite
Low mass gate:	800 Da
Digitizer start time:	19.955
Bin size:	0.5 nsec
Number of data points:	37310
Vertical scale:	500 mV
Vertical offset:	0%
Input bandwidth:	500 MHz
24	
Sample well:	100 WELL PLATE
Plate ID:	6235
Serial number:	Voyager-DE PRO
Instrument name:	CIVYAGER100 well plate,
Plate type filename:	PE Blue systems
Lab name:	
Absolute x-position:	18177.2
Absolute y-position:	37530.3
Relative x-position:	1349.67
Relative y-position:	362.81
Shots in spectrum:	200
Source pressure:	1.309e-006
Mirror pressure:	1.235e-007
TC2 pressure:	0.01248
TIS gate width:	10
TIS flight length:	689

Acquired: 15:39:00, October 15, 2002
D:\Data\HuJian\Data for burnOther samples\OCT 2002\10-15-02R\10-10423_1.digest_0004.dai
Printed: 12:15, December 17, 2002

10 / 500240

Applied Biosystems Voyager System 6235

Voyager Spec #1 [BP = 935.7, 3397]

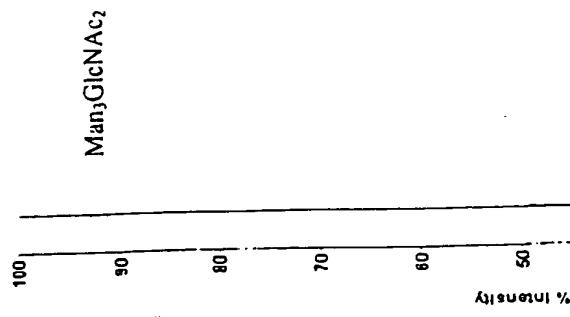


FIGURE 20

Mode of operation:	Linear
Extraction mode:	Delayed Positive
Polarity:	Positive
Acquisition Control:	Manual
3397.0	
Accelerating voltage:	20000 V
Grid voltage:	93%
Guide wire (%):	0.1%
Extraction delay time:	125 nsec
Acquisition mass range:	850 - 3200 Da
Number of laser shots:	200/spectrum
Laser intensity:	2606
Laser Rep. Rate:	20.0 Hz
Calibration type:	Default
Calibration matrix:	a-Cyano-4-hydroxydinitroanisole
Low mass Gate:	800 Da
Digitizer start time:	16.955
Bin size:	0.5 nsec
Number of data points:	37310
Vertical scale:	500 mV
Vertical offset:	0%
Input bandwidth:	500 MHz
Sampling well:	22
Plate ID:	100 WELL PLATE
Serial number:	67235
Instrument name:	Voyager DE PRO
Plate type/Name:	C:VOYAGER100 well plate
Lab name:	PE Biosystems
Absolute x position:	5516.88
Absolute y position:	37632.8
Relative x position:	-1148.67
Relative y position:	545.303
Shots in spectrum:	200
Source pressure:	6.934e-007
Min pressure:	8.466e-008
TC2 pressure:	0.01269
TIS Gate width:	10
TIS flight length:	669

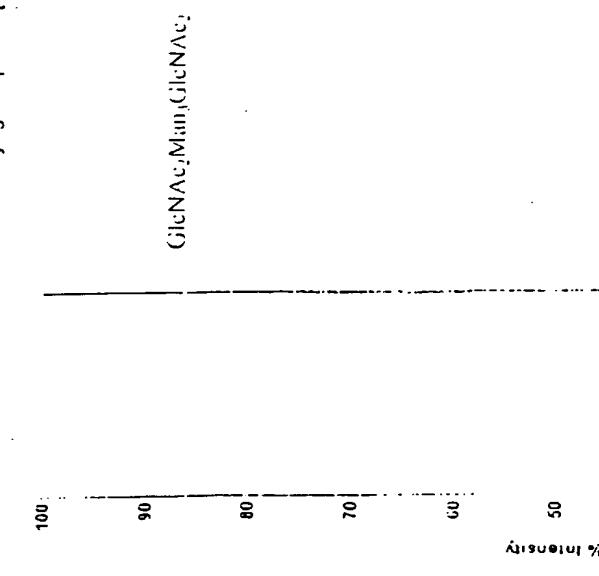
10/500240

Printed: 12:05, December 17, 2002

Acquired: 14:31:00, November 27, 2002
D:\Data\HuiJuan\Data\for burnOut\samples\NOV 2012\11-26-02\TH 11-20-02 RDP-27 hero+1,2 mannosidase_0001.dat

Applied Biosystems Voyager System 6235

Voyager Spec #1 [BP = 1356.8, 5565]



Mode of operation:	Linear
Extraction mode:	Delayed
Polarity:	Positive
Automatics control:	Automatic
Acquisition range:	20000 V
Gun voltage:	93%
Guids. wire G:	0.1%
Extraction delay time:	125 ussec
Aquisition mass range:	900 - 1200 Da
Number of laser shots:	1000-shots/shot
Laser intensity:	2802
Laser Rep. Rate:	20.0 Hz
Calibration type:	Default
Calibration mass:	a-Cyano-4-hydroxyphenylglycine, 3
Low mass galv:	875 Da
Digital start time:	20.5305
Bin size:	0.5 ussec
Number of data points:	36159
Vertical scale:	500 mV
Vertical offset:	0%
Input binwidths:	500 MHz
Laser control:	Manual
Sample positioning:	Automatic
Sample pattern:	Edge (line)
Quad storage mode:	Accumulate all passing
Bin intensity:	250
Bin intensity r:	0
Resolution:	0
Significance noise:	3
Sample well:	Y1
Plate ID:	100 WELL PLATE
Serial number:	6235
Instrument name:	Voyager DE PRO
Plate type (flextent):	CIVODYAGETR100 well plate.p
Lab Name:	PE Biosystems
Absolute x position:	1190.1
Absolute y position:	2391.25
Relative x position:	-397.403
Relative y position:	609.751
Shots in spectrum:	500
Source pressure:	9.93e-007
Mirror pressure:	9.74e-008
T/C2 pressure:	0.0122
TIS gate width:	10
TIS flight length:	600

Acquired: 12:57:00, October 28, 2002
 Sample Description: Comments:
 C:\Data\Huijuan\Data for binScreen\data\Orion\2002\IN Mass\digest 10-23-02\WFB-JN LA .mz:32 IV 10-24\U_91_0001.dat

Printed: 10:54, December 10, 2002

Applied Biosystems Voyager System 6235

Voyager Spec #1 [BP = 934.5, 7357]

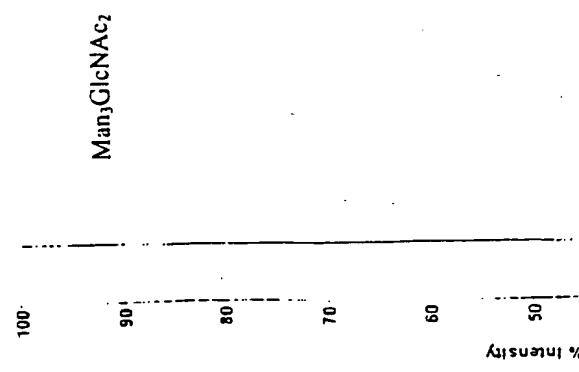


FIGURE 22

Mode of operation:	Linear
Extraction mode:	Delayed
Polarity:	Positive
Acquisition control:	Manual
Accelerating voltage:	19000 V
Grid voltage:	94%
Guide wire:	0%
Extraction delay time:	175 nsec
Acquisition mass range:	800 ... 3200 Da
Number of laser shots:	150/spectrum
Laser intensity:	3052
Laser Rep. Rate:	20.0 Hz
Calibration type:	Default
Calibration matrix:	α-Cyano-4-hydroxyphenylalanyl-L-alanine
Low mass gate:	1000 Da
Digitizer start time:	19.8945
Bin size:	0.5 nsec
Number of data points:	39555
Vertical scale:	500 mV
Vertical offset:	0%
Input bandwidth:	500 MHz
Sample well:	91
Plate ID:	100 WELL PLATE
Serial number:	6235
Instrument name:	Voyager-IE PRO
Plate Type/Name:	CIVDYGAGR100 well plate p
Lab name:	IFC Biosystems
Absolute x-position:	1843.77
Absolute y-position:	306.377
Relative x-position:	256.268
Relative y-position:	-1281.12
Shots in spectrum:	150
Source pressure:	6.671e-007
Minor pressure:	8.165e-008
TCD pressure:	0.01199
TIS gate width:	10
TIS flight length:	609

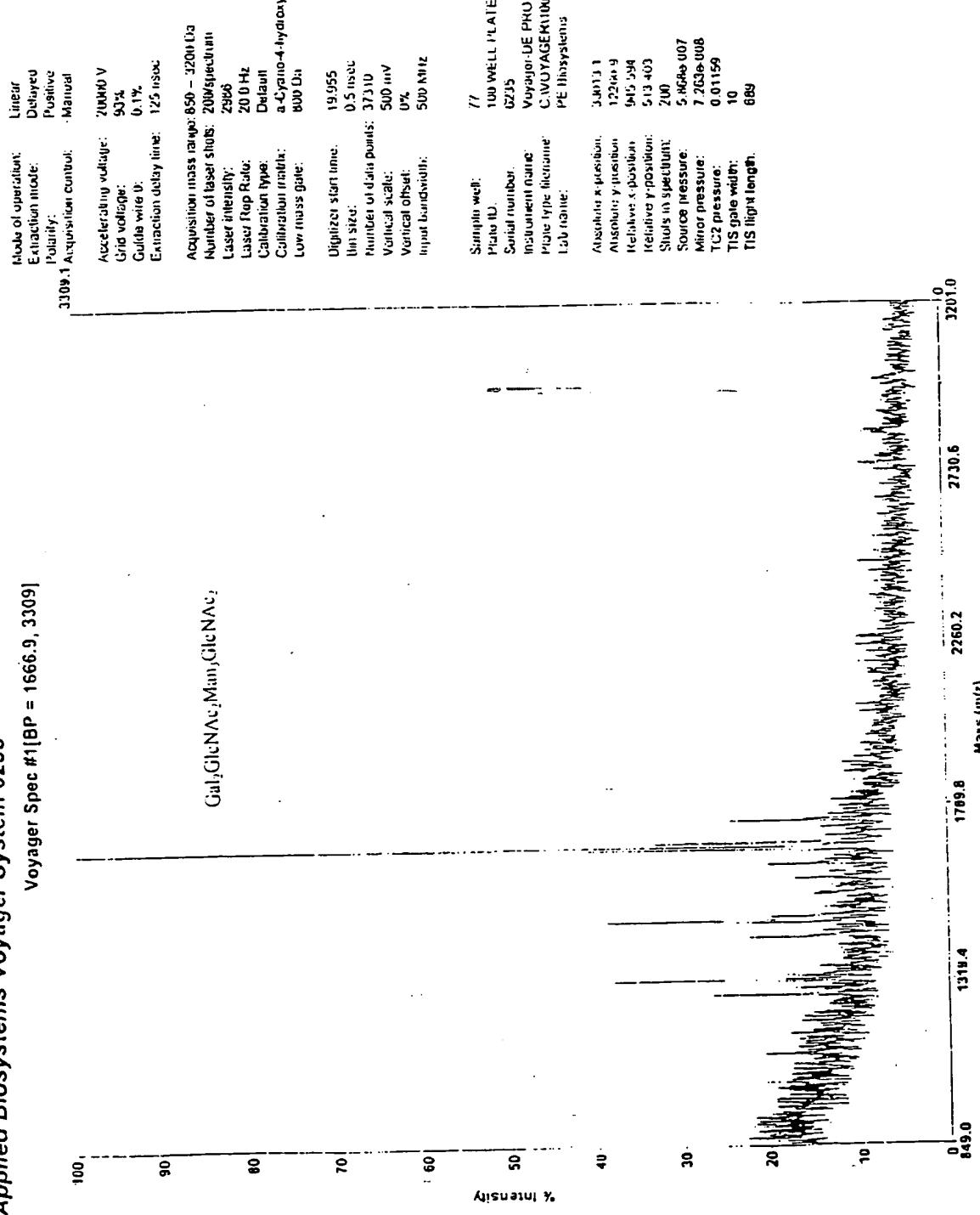
Acquired: 08-30-00, October 30, 2002

D:\Data\FullScanData for BurnScreen\data\October 2002\PPB-JN LA 30-32 1024x1024\1024x1024.mgf_0002.dat

Printed: 10:53, December 18, 200

Applied Biosystems Voyager System 6235
Voyager Spec #1(BP = 1666.9, 3309)

FIGURE 23



Acquired: 13:05:30, December 07, 2002

Printed: 11:03, December 07, 2002

Applied Biosystems Voyager System 6235
Voyager Spec #1[BP = 2264.5, 3912]

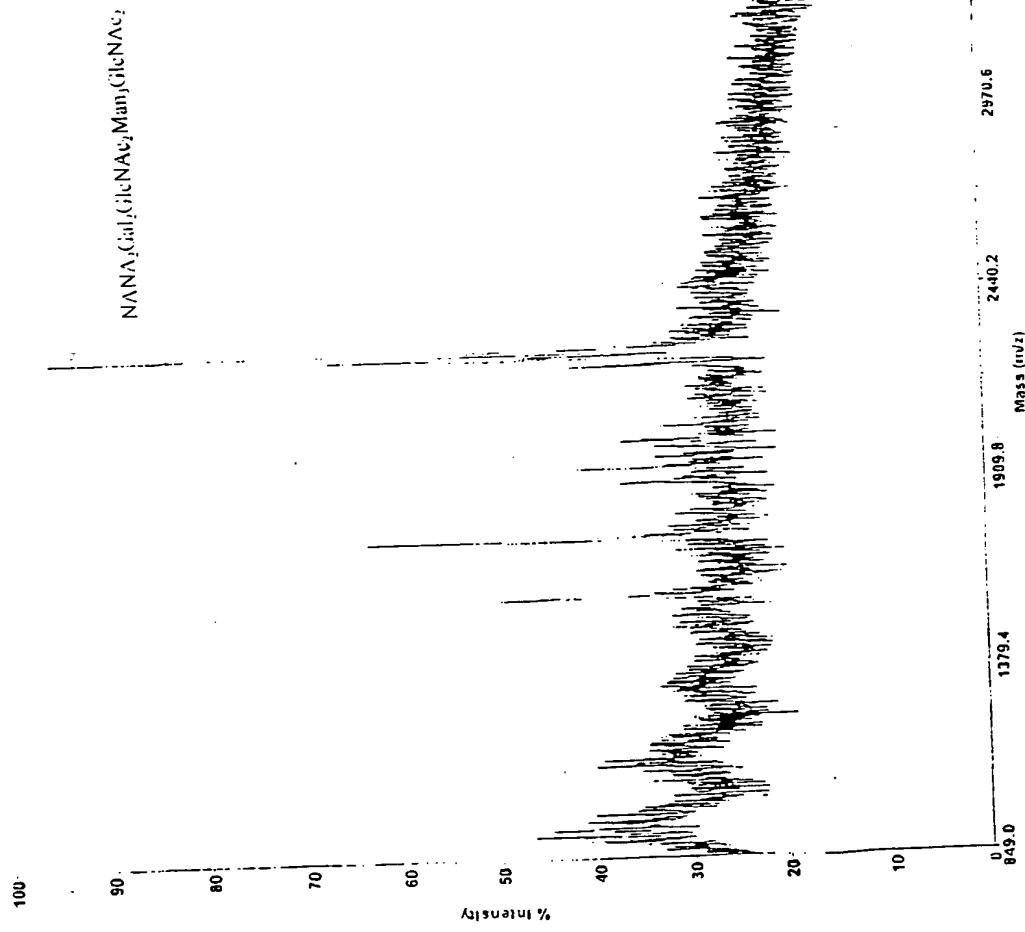


FIGURE 24

Mode of operation: Linear
Extraction mode: Delayed
Polarity: Negative
Manual

3912.0 Acquisition Control:

Accelerating voltage: 20000 V
Grid voltage: 9.5%
Gauge wire 0: 0.1%
Extraction delay time: 1.75 nsec

Acquisition mass range: 850 ... 3500 Da
Number of laser shots: 200 SpinCount
1365
Laser intensity:
20.0 Hz
Calibration type: Default
Calibration matrix: a-Crata-4-hydroxydihydroxamic acid
Low mass gate: 300 Da

Objectizer start time: 19.938
Bin size: 0.5 nsec
Number of data points: 400049
Vertical scale: 500 mV
Vertical offset: 0%
Input bandwidth: 500 MHz

Sample well: 42
Plate ID: 100 WELL PLATE
Serial number: 6215
Instrument name: Voyager DE PRO
Plate type filename: C:\VOYAGER\K10U\well_plate.p1
Lab name: PE Biosystems

Absolute x-position: 7821.04
Absolute y-position: 26536.0
Relative x-position: 1155.54
Relative y-position: -44.927
Shots in spectrum: 200
Source pressure: 7.54e-007
Minor pressure: 0.056e-008
TC2 pressure: 0.01302
TIS gate width: 10
TIS flight length: 689

Acquired: 08:47:00, December 16, 2002
D:\Data\B001\PBG-2 c siliurus_0001.dat

Printed: 11:03, December 18, 2002

FIGURE 25

S. cerevisiae ALG6

ATGGCCATTGGCAAAAGGTTACTGGTGAACAAACCAGCAGAAGAACATT
 TTATGCTTCTCCAATGTATGATTTTGATCCGTTAGGCCAGTGGGAA
 CCAATGGCTGCCAGAATATATTATCTTGATGTGCTGTAATACTGAGGTG
 CACAATTGGACTTGGTCCATTCTGGGAAAGGCAGTCCACCGCTGTACG
 GCGATTTGAGGCTCAGAGACATTGGATGAAATTACGCAACATTACCG
 CTTCTAAAGTGGTACTGGTATGATTGCAATACTGGGGATTGGACTATCCA
 CCATTAACAGCATTCTACCGTACCTCTGGGCCTAATTGGATCTTTTCA
 ATCCATCTTGGTTGCACTAGAAAAGTCACGTGGCTTGAATCCCCGATA
 ATGGCCTGAAAACATATATGCGTTACTGTCATCATTAGCGACATATTGT
 TTTACTTCCTGCAGTAATACTTAACTAAGTGGCTTGGTAGATATCGAA
 ACCAGTCGCCATAGGACAATCTATTGCGGCATCAGCGATTGTTCCAAC
 CTTCATTAATGCTCATTGACCATGGGCACCTTCATAATTCAACTGTCATGC
 TTGGCCTTACTGCTTATGCCATAAAATAACTTATTAGATGAGTATTATGCTA
 TGGCGGCCGTTGTTGCTTATCCATTGTTAAACAAATGGCATTGTA
 TTATGCACCGATTGTTGCTTATCTATTAAAGTCGATCATTGCTGTTCCCC
 AAATTAAACATAGCTAGATTGACGGTTATTGCGTTGCAACACTCGCAACT
 TTTGCTATAATATTGCGCCATTATATTCTGGGAGGGAGGATTAAAGAAT
 ATTCAACCAATGTATTACAGGATATTCCCTTGCCAGGGCATCTCGAA
 GACAAGGTTGCTAACTCTGGTGCCTACGAACGTGTTGAAATACAA
 GGAAAGATTCACTATACAACAACTCCAGCTATATTCAATTGATTGCCACCGT
 GATTGGTTCTTACCAAGCCATGATAATGACATTACTCATCCCAAAAAGCA
 TCTTCTCCCACACGTGTTAATCGCATGTTGATGTCCTTTCTTTAGC
 TTTCAAGTACATGAGAAAACATCCTCATCCCACCTTGCCATTACACTA
 CTCTACTCCTCTACTGATTGGAATGTTCTATCTCTTGAAGTTGGATAAAC
 AATGTGGCTTGTACGCTATGCCCTTGTTGAAAAGGACGGTCTTCAT
 TTACAGTATGCCGTATCTTCTTAAGCAATTGGCTATTGGAAATTTC
 AGTTTATTACACCAAGGTTCTGCCAAAATCTTAACCTCTGGCCCTTCT
 ATCAGCAGCATCAATAGCGACTATAGAAGAAGAAGCTTACTGCCATATAA
 TGTGGTTGGAAAAGTTTATCATAGGAACGTATATTGCTATTGGCTTTA
 TCATTCTTAGATCAATTGTTAGCACCTCCATCGAAATATCCAGACTGTG
 GGTGTTGTTGAACTGTGCTGTTGGGTCATTGCTTAGCATATTGGCTA
 TGGTCTTATTACAAGATATTCACTCCGGTAGCAAATCCATGAAGGACTTG
 TAG

S. cerevisiae ALG6p

MAIGKRLLVNKPAEESFYASPMYDFLYPFRPVGNQWLPEYIIFVCAVLRCTIG
 LGPYSGKGSPPLYGDFEAQRHWMEITQHLPLSKWYWYDLQYWGLDYPPPLTA
 FHSYLLGLIGSFFNPSWFALEKSRGFESPNDNLKTYMRSTVIISDILFYFPNAV
 FTKWLGRYRNQSPIGQSIAASAAILFQPSLMLIDHGHFQYNNSVMLGLTAYAINN
 LLDEYYAMAACVFLVLSICFKQMALYYAPIFFAYLLRSRSLFPKFNIARLT
 VIAFATLATFAIIAPPLYFLGGGLKNIHQCIRIFPFARGIFEDKVANFWCV
 TNVFVKYKERFTIQQLQLYSLIATVIGFLPAMIMTLHPKKHLLPYV
 LIACSMSFFLFSQVHEKTILIPLLPITLLYSTDWNVLSLVSWINNVALFT
 LWPLLKDGLHLQYA
 VSFLLSNWLNIGNFSFITPRFLPKSLTPGPSISSINSDYRRRSLLPY
 NVVVWKSFIIGTYIAMGFYHFLDQFVAPP SKYPDLWVLLNC
 AVGFICFSIFWLWSYYKIFTSGSK
 SMKDL

10/500240

FIGURE 26

P. pastoris ALG6

ATGCCACATAAAAGAACGCCCTAGCAGTCTGCTGTATGCAAGAATTCC
AGGGATCTCTTGTAAAACCTCTCCGGTGTGTTGATTTTGTCCTCTTGG
CCCGCTCCTAATCAATGGGTAGCACGATACATCATCATCATCTTGC
CTCATCAGATTGGCAGTTGGGCTGGGCTCCATTCCGGCTCAACACCC
CCAATGTATGGGGATTTGAAGCTCAGAGGCATTGGATGGAAATTACT
GCATTATCCATAGAAAAATGGTACTTCTACGACTGCAATATTGGGG
TGACTATCCTCCCTGACAGCCTTCATTCACTACTTCTTGGCAAATTAG
AGCTTCATCAATCCAGCATGGTTGCTTAGACGTCTCCAGAGGGTTG
TCAGTGGATCTAAATCGTACATGAGGGCGACCGCAATTCTCAGTGAG
GTTATGTTATTCCAGCTGTCATTGGTATTGCGTTGGATGGACTAAC
TACTTCATCAAAACGCCATTGAGCAAACATAATAGCGTCTGCTATT
TTCAATCCATCTTAATTATCATAGATCATGCCACTCCAGTACA
GTTATGCTAGGTTTGCTTATTATCCATATTAAATCTGTTGACGATAATT
TTGCAATTAGCGGCTATTTCGTTCTTCAATAAGCTTAAGCAAATGG
TCTCTATTATAGCCCCATCATGTTTTACATGCTGAGTGTGAGTTGG
CCTTGAAAAACTCAACTTGTGAGATTGGCTACTATCAGTATTGAG
CTCTTGACTTTGCAACTCTATTACTGCCTTGTATTAGTAGATGGGATGT
CACAAATTGCCAAATATTATTCAAGAGTTCCGTTCAAGAGGGCTTGT
TTGAGGATAAGGTGCCAACTTTGGTGTACAACGAATACTGGTAAAG
TACAAACAGTTATTCACTGACAAAACCCTACTAGGATATCGCTAGTAG
AACTTGATTGCAATTAGTCGTCTGCTTCATCATTTACTCACCCAAAG
AAGGTTTACTACCGTGGCTTTGCTGCTCTGGCGTTCTATCTT
TCTCTTCCAAGTCCACGAGAAATCAGTTAGTTCCATTGATGCC
CTCTATTACTGGTAGAAAAAGACTGGACATCATCTCAATGGCTGCTGG
TTCTAATATTGCCCTCTCAGCATGTGGCCTCTATTAAAAAGAGACGG
TGGCTTGGAAATATTGTCTGGAAATATTGAGTAATTGGCTGATTGG
ACCTCAATTGGATTAGTAAATGGCTGTCCCCAGTTCCCTGATTCCAG
CTACTCTCTCCAAAAAGTTCTAAAAGAGACTAAACAGTTGTT
ACTCACTGGTTTGGGGTCACTAACATTGCTTACACCTCGGAGCTACA
GTTATCCAGTTGCTAGATTGGCTGTACCTCACCTGCCAAGTATCCAG
TTGTGGGTATTGAAACACTACATTGCGTTGCTTGGTTGGTT
GGCTATGGATTAACTACAATCTGTACATTGCGTATTAAAGCTAAAG
ATGCTTAG

P. pastoris Alg6

MPHKRTPSSLLYARIPGISFENS P VFDLSPFGPAPNQWVARYIIIIFAILIRLAV
GLGSYSGFNTPPMYGDfeaQRHWMEITQHLSIEKWYFYDLQYWGLDYPPLT
AFHSYFFGKLGFinPAWFALDVSRGFESV D LKSYM RATAILSELLCFIPAVIW
YCRWMGLNYFNQNAIEQTIIASAILFNP SLI IDHGHFQYN SVM LGF ALLSILNL
LYDNF ALAAIFFVLSISFKQM ALYYSPIMFFYMLSVSCWPLKNFNLRLATISI
AVLLTFATLLPFVLVDGMSQIGQILFRVFPFSRGLFEDKVANFWCTTNILVK
YKQLFTDKTLTRISLVATLIAISPSCFIIFTHPKKVLLPWAF AAC SWAFYLFSFQ
VHEKSVLVPLMPTTLLVEKLDIISMVCWISNIAFFSMWPLLKRDGLALEYF
VLGILSNWLGNLNWISKWLVP SFLIPGPTLSKVKPKRDTKTVVH THWFWGS
VTFVSYLGATVIQFVDWLYLPPAKYPDLWVILNTLSFACFGLFWLWINYNL
YILRDFKLKDA

10/500240

FIGURE 27 (sheet 1)

P. pastoris ALG6 BLAST

Score	E	Sequences producing significant alignments:	(bits)	Value
gi 1420090 emb CAA99190.1	ORF YOR002w [Saccharomyces cerev... 489		e-137	
gi 7490584 pir T40396	glucosyltransferase - fission yeast ... 369		e-101	
gi 19921070 ref NP_609393.1	CG5091-PA [Drosophila melanoga... 47		4e-64	
gi 15240920 ref NP_198662.1	glucosyltransferase-like prote... 244		3e-63	
gi 7019325 ref NP_037471.1	dolichyl-P-Glc:Man9GlcNAc2-PP-d... 238		2e-61	
gi 12002040 gb AAG43163.1 AF063604_1	brain my046 protein [H... 236		7e-61	
gi 1176671 sp Q09226 ALG6 CAEEL	Probable dolichyl pyrophosp... 222		9e-57	
gi 21302638 gb EAA14783.1	agCP4617 [Anopheles gambiae str.... 219		8e-56	
gi 5441788 emb CAB46771.1	probable glucosyltransferase [Sc... 192		1e-47	
gi 13129070 ref NP_076984.1	hypothetical protein MGC2840 s... 112		1e-23	
gi 2996578 emb CAA12176.1	glucosyltransferase [Homo sapiens] 112		1e-23	
gi 20835439 ref XP_131506.1	similar to Dolichyl pyrophosph... 104		3e-21	

Alignments

S. cerevisiae

Score = 489 bits (1259), Expect = e-137
 Identities = 274/530 (51%), Positives = 358/530 (67%), Gaps = 5/530 (0%)

Query: 20 SFENSPVFDLSPFGPAPNQWVXXXXXXXXXXXXXVGLGSYSFGNTPPMYGDFEAQRH 79
 SF SP++DFL PF P NQW+ +GLG YSG +PP+YGDFEAQRH
 Sbjct: 16 SFYASPMYDFLYPFRPVGNQWLPEYIIFVCAMILRCTIGLGPYSGKGSPPLYGDFEAQRH 75

Query: 80 WMEITQHLSIEKWYFYDLQYWGLDYPPLTAFHSYFFGKLGSPINPAWFALDVSRGFESVD 139
 WMEITQHL + KKY+YDLQYWGLDYPPLTAFHSY G +GSF NP+WFAL+ SRGFES D
 Sbjct: 76 WMEITQHLPPLSKWYWDLQYWGLDYPPLTAFHSYLLGLIGSFFNPSWFALEKSRGFESPD 135

Query: 140 --LKSYSMRATAILSELLCFIPAVIWYCRWMGLNYFNQNAIEQTIIASAILFNPSLIIIDH 197
 LK+YMR+T I+S++L + PAVI++ +W+G Y NQ+ I Q+I ASAILF PSL++IDH
 Sbjct: 136 NGLKTYMRSTVIISDILFYPPAVIYFTKWLG-RYRNQSPIGOSIAASAILFQPSLMLIDH 194

Query: 198 GHFQYNSVMLGFALLSILNLLYDNFALAAIFFVLSISFKQMALYYSPIMFFYMLSVSCWP 257
 GHFQYNSVMLG +I NLL + +A+AA+ FVLSI FKQMALYY+PI F Y+LS S
 Sbjct: 195 GHFQYNSVMLGLTAYAINNLDEYYAMAACFVLSICFKQMALYYAPIFFAYLLSRSL- 253

Query: 258 LKNFNLLRLATISIAVLLTFATLLP-FVLVDGMSQIGQILFRVFPFSRGLFEDKVANFW 316
 FN+ RL I+ A L TFA + P + L G+ I Q + R+FPF+RG+FEDKVANFW
 Sbjct: 254 FPKFNIARLTIVAFATLATFAIIFAPLYFLGGGLKNIHQCIHRIFPFARGIFEDKVANFW 313

Query: 317 CTTNILVKYKQLFTDKTLTRISLVATLIAISPSCFIIFTHPKKVLLPWAFAACSWAFYLF 376
 C TN+ VKYK+ FT + L SL+AT+I P+ + HPKK LLP+ ACS +F+LF
 Sbjct: 314 CVTNVFVKYKERFTIQQLQLYSLIATVIGFLPAMIMTLLHPKKHLLPYVLIACSMSFFLF 373

Query: 377 SFQVHEKSXXXXXXXXXXXXKLDIISMVCWIISNIAFFSMWPLLKRDGIALEYFVLGI 436
 SFQVHEK+ D +++S+V WI+N+A F++WPLLK+DGL L+Y V +
 Sbjct: 374 SFQVHEKTIILIPLLPITLLYSSTDWNVLSLVSWINNVALFTLWPLLKKDGLHLQYAVSFL 433

Query: 437 LSNWLIGNLNWISKWLVPFLIPGPTLSKKVPKRDTKTVVHTHWFWGSVTFSYLGATVI 496
 LSNWLIGN ++I+ +P L PGP++S +++++ + W S +Y+
 Sbjct: 434 LSNWLIGNFSFITPRFLPKSLTPGPSISSINSDYRRRSLLPYNVVWKSFIIGTYIAMGY 493

FIGURE 27 (sheet 2)

Query: 497 QFVDWLYLPPAKYPDLWVILNTTLSFACFGLFWLWINYNLYILRDFKLKD 546
 F+D PP+KYPDLWV+LN + F CF +FWLW Y ++ +KD
 Sbjct: 494 HFLDQFVAPP SKYPDLWVLLNCAVGFICFSIFWLWSYYKIFTSGSKSMKD 543

S. pombe

Score = 369 bits (946), Expect = e-101
 Identities = 228/513 (44%), Positives = 315/513 (61%), Gaps = 35/513 (6%)

Query: 21 FEN-SPVFDFLSPFGPAPNQWVXXXXXXXXXXXXXVGLGSYSGFNTPPMYGDFEAQRH 79
 FEN +PV F+S F +*** + +G YSG+NTPPMYGDFEAQRH
 Sbjct: 5 FENGAPVQQFVSRFRSYSSKFLFPCLIMSLVFMQWLISIGPYSGYNTPPMYGDFEAQRH 64

Query: 80 WMEITQHLSIEKWYFYDLQYWGLDYPLTAFHSYFFGKLGS-FINPAWFALDVSRGFESV 138
 WME+T H + +WYF DLQ+WGLDYPLTA+ S+FFG +G F NP WFA SRGFES+
 Sbjct: 65 WMELTLHTPVSQWYFRDLQWGLDYPLTAYVSWFFGIIGHYFFNPEWFADVTSRGFESL 124

Query: 139 DLKSYM RATAILSELLCFIPAVIWYCRWMGLNYFNQNAIEQTIIASAILFNPSLIIIDHG 198
 +LK +MR+T I S LL +P +**Y +W N +** +LF P+L++IDHG
 Sbjct: 125 ELKLFMRSTVIASHLLLIVPPLMFYSKWWSSRRI--PNFVDRNASLIMVLFQPALLIDHG 182

Query: 199 HFQYNSVMLGFALLSILNLLYDNFALAATFEVLSISFKQM ALYYSPIMFFYMLSVCWPL 258
 HFQYNS VMLG + +I NLL + + A FF L+**FKQM ALY++P +FY+L P
 Sbjct: 183 HFQYNCVMLGLV MYAIANLLKNQYVAATFFFCLALTFKQM ALYFAPP IFYLLGTCVKPK 242

Query: 259 KNFNLLRLATISIAVLLTFATLLPFVLVDGMSQIGQILFRVFPFSRGLFEDKVANFWCT 318
 F+ R +S+ V+ TF+ +L P++ +D + QIL RVFPF+RGL+EDKVANFWCT
 Sbjct: 243 IRFS--RFILLSVTVVFTFSLILFPWIYMDYKTLLPQILHRVFPFARGLWEDKVANFWCT 300

Query: 319 TNILVKYKQLFTDKTLTRISLVATLIAISPSCFIIFTHPKKVLLPWAFACSWAFYLFSF 378
 N + K +**FT L ISL+ TLI+I PSC I+F +P+K LL FA+ SW F+LFSF
 Sbjct: 301 LNTVFKIREVFTLHQLOQVISLIFTLISILPSCVILFLYPRKRLLALGFASASWGFFLFSF 360

Query: 379 QVHEKSXXXXXXXXXXXXXKDLDIISMVCWI SINIAFFSMWPLLKRDGLALEYFVLGILS 438
 QVHEKS + + +N+A FS+WPLLK+DGL L+YF L ++
 Sbjct: 361 QVHEKS VLLPLLPTSILLCHGNITT KPWIALANNLAVFSLWPLLKKDGLQYFTL VLMW 420

Query: 439 NWLIGNLNWISKWLVPSTSFLIPGPTLSKKVPKRDTKTVVHTHWFWGSVTFVSYLGATVIQF 498
 NW IG++ SK ++ F + Y+G VI
 Sbjct: 421 NW-IGDMVVFSKNVLFRF-----IQLSFYVGMI VLG 451

Query: 499 VDWLYLPPAKYPDLWVILNTTLSFACFGLFWLW 531
 +D PP++YPDLWVILN TLSFA F +LW
 Sbjct: 452 IDLFIPPPSRYPDLWVILNVTLSFAGFFT IYLW 484

D. melanogaster

Score = 247 bits (630), Expect = 4e-64
 Identities = 175/490 (35%), Positives = 267/490 (54%), Gaps = 55/490 (11%)

Query: 57 VGLGSYSGFNTPPMYGDFEAQRHW MEITQHLSIEKWYF---YDLQYWG LDYPLTAFHS 112
 + L SYSGF++PPM+GD+EAQRHW EIT +L++ +WY DLQYWG LDYPLTA+HS
 Sbjct: 19 ISLYSYSGFDSPPMHG DYEAQRHWQEITVNLAVGEWYTNSSNNLQYWG LDYPLTAYHS 78

Query: 113 YFFGKLGSFINPAWFALDVSRGFESVDLKSYM RATAILSELLCFIPAVIWYCRWMGLNYF 172
 Y G++G+ I+P + L SRGFES + K +MRAT + +**L ++PA++ + +
 Sbjct: 79 YLVGRIGASIDPRFVELHKSRGFESKEH KRFMRATVVSADVLIYLPAMLLAYSLDKAFR 138

10/500240

FIGURE 27 (sheet 3)

Query: 173 NQNAIEQTIIASAILFNPSLIIIDHGHFQYNSVMLGFALLSILNLLYDNFALAAIFFVLS 232
+ + + + + A P + ID+GHFQYN++ LGFA ++ I + L F AA FF L+
Sbjct: 139 SDDKLFLLFTLVAAY-- PGQTLIDNGHFQYNNISLGFAAVAAIAILRRRFYAAAFFFTLA 195

Query: 233 ISFKQMALYYSPIMFFYMLSVSCWPLKNFN-- LLRLATISIAVLLTFATLLPFVLVDGM 290
++ + KQM LY+S + FF L C K+F + + I+ VL TFA L + P+ + +
Sbjct: 196 LNYKQMELYHS-LPFFAFLLGECVSQKSFASFIAEISRIAAVVLGTFAILWVPW-- LGSL 252

Query: 291 SQIGQILFRVFPFSRGLFEDKVANFWCTTNILVKYKQLFTDKTLTRISLVATLIAISPSC 350
+ Q+L R+FP +RG+FEDKVAN WC N++ K K+ ++ + + + TLIA P+
Sbjct: 253 QAVLQVLHRLFPVARGVFEDKVANVWCNAVNVWKLKKHISNDQMALVCIACTLIASLPTN 312

Query: 351 FIIFTHPKVLLPWAFACSWAFYLFSFQVHEKSXXXXXXXXXXXXEKLDIISMVCW- 409
++ F V A S AF+LFSFQVHEK+ + + CW
Sbjct: 313 VLLFRRRTNVGFLLALFNTSLAFFLFSFQVHEKTILLTALPA-----LFLLKCWP 362

Query: 410 -----ISNIAFFSMWPLLKRDGLALEYFVLGILSNWLIGNLNWISKWLVPFLIPGPTLS 464
+ FSM PLL RD L + V + + + + SK LS
Sbjct: 363 DEMILFLEVTVFMSMLPLLARDELLVPAVVATVAFHLIFKCFDSKSK-----LS 410

Query: 465 KKVPKRDTKTVVHTHWFGSVTFSYLGATVIQFVDWLYLP-PAKYPDWLWVILNTTLSFA 523
+ P + + + + S + A+ L + P P KYPDLW ++ + S
Sbjct: 411 NEYPLKYIANI-----SQILMISVVVAS-----LTPVAPTKYPDLWPLIISVTSCG 456

Query: 524 CFGLFWLWIN 533
F LF+LW N
Sbjct: 457 HFFLFFLWGN 466

A. thaliana

Score = 244 bits (622), Expect = 3e-63
Identities = 187/488 (38%), Positives = 248/488 (50%), Gaps = 39/488 (7%)

Query: 62 YSGFNTPPMYGDFEAQRHWMEITQHLSIEKWY---FYDLQYWGLDYPPLTAFHSYFFGK 117
YSG PP +GDFEAQRHWMEIT +L + WY + DL YWGLDYPPLTAFHSYFFGK 117
Sbjct: 61 YSGAGIPPKFGDFEAQRHWMEITTNLPVIDWYRNGTYNDLTYWGLDYPPLTAYQSYIHGI 120

Query: 118 LGSFINPAWFALDVSRGFESVDLKSYMRATAILSELLCFIAPAVIWYCRWMGLNYFNQNAI 177
F NP AL SRG ES K MR T + S+ F PA +++ N
Sbjct: 121 FLRFFNPESVALLSSRGHESYLGKLLMRWTVLSSDAFIFFPAALFFVLFVYHRNRTRGGKS 180

Query: 178 EQTIIASAILFNPSLIIIDHGHFQYNSVMLGFALLSILNLLYDNFALAAIFFVLSISFKQ 237
E + IL NP LI+IDHGHFQYN + LG + + I + L ++ L + F L++S KQ
Sbjct: 181 EVAWHIAMILLNPCLILIDHGHFQYNCISLGLTVGAIAAVLCESEVLTCVLFLSALSHKQ 240

Query: 238 MALYYSPIMFFYMLSVSCWPLKNFNLLRLATISIAVLLTFATLLPFVLVDGMSQIGQIL 297
M+ Y++P F ++L C K+ +L + + IAV++TF P+ V + +L
Sbjct: 241 MSAYFAPAFFSHLLG-KCLRRKS-PILSVIKLGIAVITFVIFWWPY--VHSLDDFLMVL 296

Query: 298 FRVFPFSRGLFEDKVANFWCTTNILVKYKQLFTDKTLTRISLVATLIAISPSCFIIFTHP 357
R+ PF RG++ED VANFWCTT+IL+K+K LFT ++L ISL AT++A PS P
Sbjct: 297 SRLAPFERGIYEDYVANFWCTTSILIKWKNLFTTQSLKSISLAATILASLPSMVQQILSP 356

Query: 358 KKVL LPWAFAACSWAFYLFSFQVHEKSXXXXXXXXXXXXEKLDIISMVCWISNIAFFS 417
+ S AFYLF SFQVHEKS L + ++ A FS
Sbjct: 357 SNEGFLYGLLNSSMAFYLF SFQVHEKSILMPFLSATLLA---LKLPDHFSHLTYYALFS 412

10 / 500240

FIGURE 27 (sheet 4)

Query: 418 MWPLLKRDGLALEYFVLGILSNWLI---GNLNWISKWLVPNFL---IPGPTLSKKVPKRD 471
M+PLL RD L + Y L L + GN + I K V F PG
Sbjct: 413 MFPLLCRDKLLIPYLTLFLFTVIYHSPGNHHAIQKTDVSFFSKNFPGYVF----- 464

Query: 472 TKTVVHTHWFWGSVTFVSYLGATVIQFVDWLYLPPAKYPDLWVILNTTLSFACFGFWLW 531
++ TH+F V V YL PP KYP L+ L L F+ F +
Sbjct: 465 ---LLRTHFFISVVLHVLYLTIK-----PPQKYPFLFEALIMILCFSYFIMFAFY 511

Query: 532 INYNLYIL 539
NY + L
Sbjct: 512 TNYTQWTL 519

10/500240

FIGURE 28

K. lactis ALG6

ATCTCTGTTCAACAGCTCTGCATTGATTGGTCTTCGGTCCAATCTATA
TCTTGGAGGATACAAGAACCTAGTGCAATCAATGCACAGGATTTCAT
TTGCCAGGGTATCTTGAAAGATAAAGTTGCGAATTGGTGCCTTCTA
ATATTTCATCAAATATAGAAATCTATTCACTCAGAAGGATCTTCAATTAT
ACTCATTACTCGCAACAGTTATTGGGCTTACCATCATTATAACAT
TTTATACCGAAGAGACATTACTACCATATGCTTGGCCGCATGTTCGA
TGTCTTCTTATTCACTCCAGGTTCATGAAAAGACAATCTTATTAC
CTTACTCCTATTACACTCTGTACACGTCAAGAGAGATTGGAATGTTCTAT
CATTGGTTGTTGGATTAACAACGTGGCATTGTTACACTCTGGCCATTAC
TGAAAAAGGACAATCTAGTATTGCAATATGGAGTCATGTTCATGTTAGC
AATTGGTTGATCGGTAACTCAGTTCGTCACACCACGCTCCTCCCCAAA
TTTTGACACCAGGCCATCCATCAGTATAGATGTTGATTATAGACGG
GCAAGTTACTACCCAAGAGCCTAATATGGAGATAATCATTGTTGGCTCA
TATATTGCAATGGGGATTATTCACTTCTAGACTATTACGTCTCCCCGCCA
TCAAAATACCTGATTATGGGTGCTGCCAATTGTTCTGGCTCTCA
TGTTTGTGACATTGGATATGGAACAATTATAATTATCGAAATGAGAA
ACAGCACTTGCAAGATTAA

K. lactis Alg6p

ISVSTALAFIGSFGPIYIFGGYKNLVQSMHRIFPFARGIFEDKVANFWCVSNIFIK
YRNLFHQKDLQLYSLLATVIGLLPSFIITFLYPKRHLLPYALAACSMSFFLFSFQ
VHEKTILLPLLPITLLYTSRDWNVLVCWINNVALFTLWPLLKKDNLVLQYG
VMFMFSNWLNFSFVTPRFLPKFLTPGPSISIDVDYRRASLLPKSLIWRLIIV
GSYIAMGIIHFLDYYVSPPSKYPDLWVLANCISLGFCVTFWIWNNNYNSKZE
TALCKI

10/500240

FIGURE 29 (sheet 1)

K. lactis ALG6 BLAST

Score	E			
Sequences producing significant alignments:			(bits)	Value
gi 1420090 emb CAA99190.1	ORF YOR002w	[Saccharomyces cerev...	392	e-108
gi 7490584 pir T40396	glucosyltransferase - fission yeast	...	187	2e-46
gi 15240920 ref NP_198662.1	glucosyltransferase-like prote...	...	117	2e-25
gi 7019325 ref NP_037471.1	dolichyl-P-Glc:Man9GlcNAc2-PP-d...	...	103	2e-21
gi 12002040 gb AAG43163.1 AF063604_1	brain my046 protein [H...	...	102	8e-21
gi 19921070 ref NP_609393.1	CG5091-PA [Drosophila melanoga...	...	101	1e-20

Alignments

S. cerevisiae

Score = 392 bits (1006), Expect = e-108
Identities = 182/280 (65%), Positives = 218/280 (77%), Gaps = 1/280 (0%)
Frame = +1

Query: 1	ISVSTALAFIGSFGPIYIFGG-YKNLVQSMHRIFPFARGIFEDKVANFWCVSNIFIKYRN	177
	I+ +T F F P+Y GG KN+ Q +HRIFPFARGIFEDKVANFWCV+N+F+KY+	
Sbjct: 265	IAFATLATFAIIIFAPLYFLGGGLKNIHQCIHRIFPFARGIFEDKVANFWCVTNVFKYKE	324
Query: 178	LFTQKDLQLYSLLATVIGLLPSFIITFLYPKRHLLPYALAAACSMSFFLFSFQVHEKXXXX	357
	FT + LQLYSL+ATVIQ LP+ I+T L+PK+HLLPY L ACSMSFFLFSFQVHEK	
Sbjct: 325	RFTIQQLQLYSLIATVIGFLPAMIMTLLHPKKHLLPYVLIACCSMSFFLFSFQVHEKTILI	384
Query: 358	XXXXXXXXXXYTSRDWNVLSQLVCWINNVALFTLWPLLKKDNLVQYGVMFMFSNWLNIGNFSF	537
	Y+S DWNVLSLV WINNVALFTLWPLLKKD L LQY V F+ SNWLIGNFSF	
Sbjct: 385	PLLPITLQLYSLSTDWNVLSQLVSWINNVALFTLWPLLKKDGHLQYAVSFLLSNWLIGNFSF	444
Query: 538	VTPRFLPKFLTPGPSISIDVDYRRASLLPKSLIWRLLIVGSYIAMGIIHFLDYYVSPPS	717
	+TPRFLPK LTPGPSIS I+ DYRR SLLP +++W+ I+G+YIAMG HFLD +V+PPS	
Sbjct: 445	ITPRFLPKSLTPGPSISSINSDYRRSLLPYNVVVWKSFIIGTYIAMGFYHFLDQFVAPPS	504
Query: 718	KYPDLWVLANC SLGFSCVT FWIWN NYXL FEMRN STLQDL	837
	KYPDLWVL NC++GF CF FW+W+ Y +F + +++DL	
Sbjct: 505	KYPDLWVLLNC AVGFICFSI FWLWSYYKIFTSGSKSMKDL	544

S. pombe

Score = 187 bits (475), Expect = 2e-46
Identities = 106/280 (37%), Positives = 150/280 (53%), Gaps = 1/280 (0%)
Frame = +1

Query: 1	ISVSTALAFIGSFGPIYIFGGYKNLV-QSMHRIFPFARGIFEDKVANFWCVSNIFIKYRN	177
	+SV+ F P +I+ YK L+ Q +HR+FPFARG++EDKVANFWC N K R	
Sbjct: 251	LSVTVVFTFSLILFP-WIYMDYKTLLPQILH RVFPFARGLWEDKVANFWCTLNTVFKIRE	309
Query: 178	LFTQKDLQLYSLLATVIGLLPSFIITFLYPKRHLLPYALAAACSMSFFLFSFQVHEKXXXX	357
	+FT LQ+ SL+ T+I +LPS +I FLYP++ LL A+ S FFLFSFQVHEK	
Sbjct: 310	VFTLHQLQVISLIFTLISILPSCVILFLYPRKRL ALGFASASWGFFLFSFQVHEKVLL	369

10/500240

FIGURE 29 (sheet 2)

Query: 358 XXXXXXXXYTSRDWNVLSLVCWINNVALFTLWPLLKKDNLVLQYGVFMFSNWLNIGNFSF 537
+ + NN+A+F+LWPLLKKD L L QY + + NW
Sbjct: 370 PLLPTSILLCHGNITTKPWIALANNLAVFSLWPLLKKDGLGLQYFTLVLWMNW----- 422

Query: 538 VTPRFLPKFLTPGPSISIDVDYRRASLLPKSLIWRLIIIVGSYIAMGIIHFLDYYVSPPS 717
I D+ V K+++R I + Y+ M +I +D ++ PPS
Sbjct: 423 -----IGDMVV-----FSKNVLFRFIQLSFYVGMIYLGIDLFI PPPS 460

Query: 718 KYPDLWVLANCMSLGFSCFVTFWIWNNTYXLFEMRNSTLQDL 837
+YPDLWV+ N +L F+ F T ++W L + + DL
Sbjct: 461 RYPDLWVLNVTLSFAGFFTIYLWTLGRLLHISSKLSTDL 500

A. thaliana

Score = 117 bits (292), Expect = 2e-25
Identities = 81/240 (33%), Positives = 120/240 (50%), Gaps = 2/240 (0%)
Frame = +1

Query: 85 MHRIFPFARGIFEDKVANFWCVSNIFIKYRNLFTQKDLQLYSLLATVIGLLPSFIITFLY 264
+ R+ PF RGI+ED VANFWC ++I IK++NLFT + L+ SL AT++ LPS + L
Sbjct: 296 LSRLAPFERGIYEDYVANFWCTTSILIKWKNLFTTQSLKSISLAATILASLPSMVQQILS 355

Query: 265 PKRHLLPYALAAACMSFFLFSFQVHEKXXXXXXXXXXYSRDWNVLSLVCWINNVALF 444
P Y L SM+F+LFSFQVHEK + L + ALF
Sbjct: 356 PSNEGFLYGLLNSSMAFYLFQVHEKSILMPFLSATLLALKLPDHFSHLTYY---ALF 411

Query: 445 TLWPLLKKDNLVLQYGVFMFSNWLNIGNFSFVTPRFLPKFLTPG--PSISIDVDYRRAS 618
+++PLL +D L++ Y + SF+ F + +PG +I DV +
Sbjct: 412 SMFPLLCRDKLLIPYLTL-----SFL---FTVIYHSPGNHHAIQKTDVSFFSFK 457

Query: 619 LLPKSLIWRLIIIVGSYIAMGIIHFLDYYVSPPSKYPDLWVLANCMSLGFSCFVTFWIWNNTY 798
P + L+ +I++ ++H L + PP KYP L+ L FS F+ F + NY
Sbjct: 458 NFFPGYVF--LLRTHFFISV-VLHVLYLTICKPPQKYPFLFEALIMILCFSYFIMFAFYTNY 514

H. sapiens

Score = 103 bits (258), Expect = 2e-21
Identities = 78/266 (29%), Positives = 123/266 (46%), Gaps = 3/266 (1%)
Frame = +1

Query: 7 VSTALAFIGSGFGPIYI--FGGYKNLVQSMHRIFPFARGIFEDKVANFWCVSNIFIKYRNL 180
V A + SF ++ F + +Q + R+FP RG+FEDKVAN WC N+F+K +++
Sbjct: 232 VKLACIVVASFVLCWLPPFTEREQTLQVLRRLFPVDRGLFEDKVANIWCFSNVFLKIKDI 291

Query: 181 FTQKDLQLYSLLATVIGLLPSFIITFLYPKRHLLPYALAAACMSFFLFSFQVHEKXXXXX 360
+ + S T + LLP+ I L P + L + C++SFFLFSFQVHEK
Sbjct: 292 LPRHIQLIMSFCFTFLSLLPACIKLILQPSSKGFKFTLVSCALSFFLFSFQVHEKSILLV 351

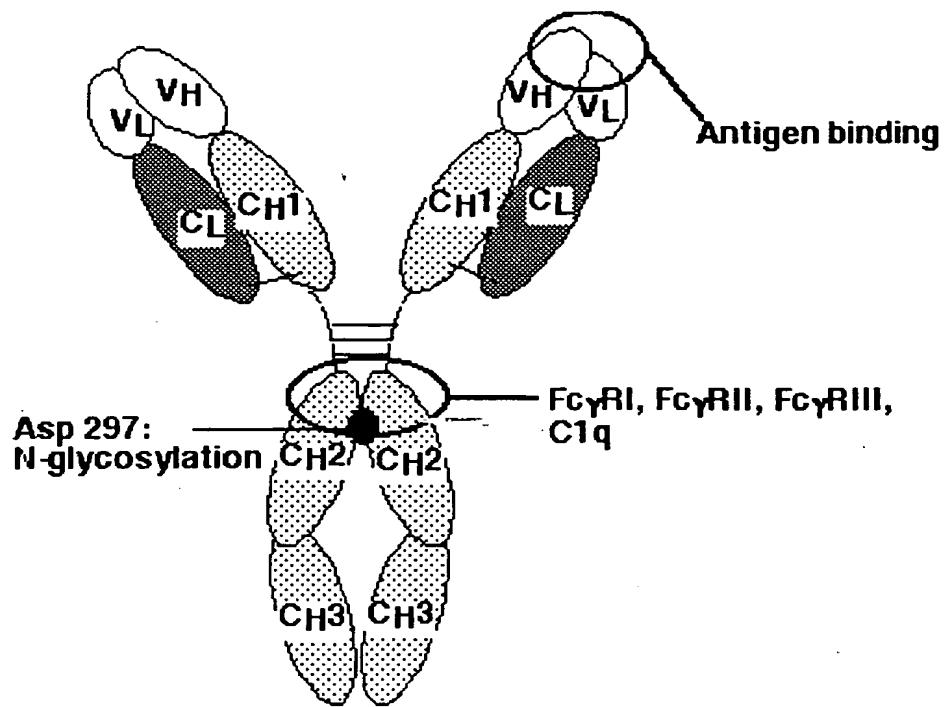
Query: 361 XXXXXXXYTSRDWNVLSLVCWINNVALFTLWPLLKKDNLVLQYGVFMFM-FSNWLIGNFSF 537
+ + + W V+ F++ PLL KD L++ V M F + +FS
Sbjct: 352 SLPVCLVLS----EIPFMSTWFLLVSTFSMLPLLLKDELLMPSVTTMAFFIACVTSFSI 407

Query: 538 VTPRFLPKFLTPGPSISIDVDYRRASLLPKSLIWRLIIIVGSYIAMGIIHFLDYYVSPPS 717
+ SIS V S I + + + S I M ++ + + PP
Sbjct: 408 FEKTSEEELQLKSFSIS---VRKYLPCFTFLSRIIQYLFISVITMVLTLMTVTLDPPQ 464

Query: 718 KYPDLWVLANCMSLGFSCFVTFWIWNNTY 795
K PDL+ + C + F+ F ++ N
Sbjct: 465 KLPDLFSVLVCFVSCLNFLFFLVYFN 490

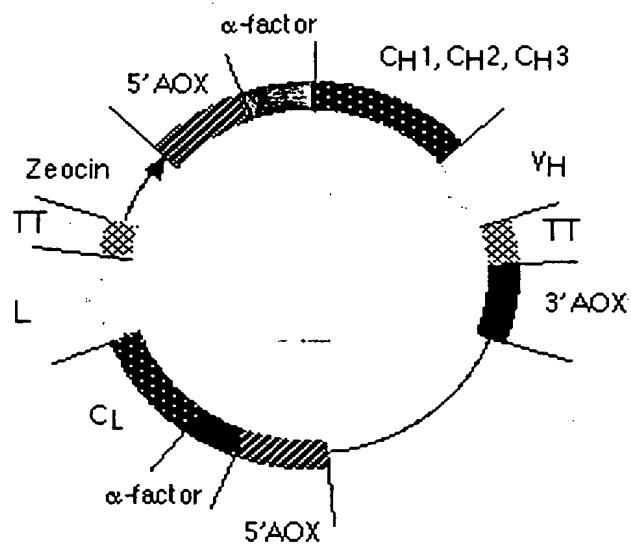
10/500240

FIGURE 30



10/500240

FIGURE 31



10/500240

FIGURE 32

>gi|6754685|ref|NM_010795.1| Mus musculus mannoside acetyl glucosaminyltransferase 3 (Mgat3), mRNA

ATGAAGATGAGACGCTACAAGCTCTTCTCATGTTCTGTATGGCTGGCCTGTGCCCTCATATCCTTCCTGC
ACTTCTTAAGACCTTATCCTATGTCACCTTCCCGAGAGAACTGGCTCCCTCAGCCCTAACCTCGTATC
CAGCTTCTCTGGAACAATGCCCCGTCACTCCCCAGGCCAGTCCGGAGCCGGGTGGCCCCGACCTATTG
CGGACACCCCTCTACTCCCACCTCTCCCTGCTCAGCCACTGTCCCCGAGCAAGGCCACAGAGGAACGTG
ACCGGGTGGACTCTGTGTTGCCGGAGGACACCACGGAGTATTTGTGCGCACCAAAGCTGGTGGTGTG
CTTCAAACCAGGTACCGAGATGCTGGAGAACCTTCGCCAGGGCGACAGAGGAGAAGCCGAAGTGTCT
GAGGGCTCTCAGCCCCGGGACCTGCTCGGAGGCCATGAGGCACGTGTTGAGTACGCGGGAGCGCTGG
GCAGCCGGGGACTAGGCGAACGTGGTTGAGTGTGTGCCCTGCCAGGCTGGCACGGGCCAGTTCGG
GGTCCCCACGGTGGTGCAGTATTCCAACCTGCCACCAAGGAACGCCCTGGTACCCAGGGAGGTACCGAGG
CGGGTTATCAACGCCATCAACATCAACCACGAGTCGACCTGCTGGATGTGCGCTTCCATGAGCTGGAG
ATGTTGTGGACGCCCTCGTGGTCTGTAATCTAATTCAACGCCCTACGGGAGGCCCTGCCCTCAAGATT
CCGAGAGATGCTGACCAATGGCACCTCGAGTACATCCGCCAACAGGTGCTCTATGTCCTGGACCAT
TTCCCACCTGGTGGCGTCAGGACGGCTGGATTGCGGATGACTACCTGCGCACCTTCCTCACCCAGGATG
GCGTCTCCCCTCGCGAACCTCGGGCCGATGACGTCTTATCATCGACGATGCGGACGAGATCCCTGC
GCGTGTGGTGTGCTGTTCTCAAACCTACGATGGCTGGACAGAGCCCTCGCCTTCCACATGCGGAAG
TCCCTGTATGGTTCTCTGGAACAGCAGCCGGCACACTGGAGGTGGTGTGCAAGGCTGCACCATGGACATGC
TGCAGGCCGTGTATGGGCTGGATGGCATCCGCTCGGCCAGTACTACACCATGCCAACCTTCG
GCAGTATGAGAACCGCACCGGCCACATCCTAGTGCAGTGGCTCTCGGAGCCCCCTGCACTTCGCGGC
TGGCATTGCTCTGGTGTTCACACCCGAGGGCATCTACTTAAACTCGTGTGCAAGCCAGAATGGCGACT
TCCCCCGCTGGGGTGAATATGAGGACAAGAGGGACCTCAATTACATCCGAGCTTGATCCGACTGGGG
ATGGTTGACGGAACGCAGCAGGAGTACCCCTCTCGGAGCCAGTGAGCACATGTATGCTCTAAATAC
CTGCTCAAGAACTATGACCAGTCCGCTACTTGCTGGAAAATCCCTACCGGGAGCCAAGAGCACTGTAG
AGGGTGGGCCAGAACAGGGCTCAGATGGAAGGCCATCTGCTGCAAGGGCAAGTTGGATACAGTGG
GGGCTAG

>gi|2117717|pir||JC4362 beta-1,4-mannosyl-glycoprotein 4-beta-N-acetylglucosaminyltransferase (EC 2.4.1.144) III - mouse
MRRYKLFLMFCMAGLCLISFLHFFKTLSYVTFPRELASLPNLISSFWNNAPVTPQASPEPGDPDLLRT
PLYSHSPLLQPLSPSKATEELHRVDFVLPEDTTEYFVRTKAGGVCFKPGTRMLEKPSPGRTEEKTEVSEG
SSARGPARRPMRHVLSSRERLGSRGTRRKWVECVCLPGWHGPSCGVPTVVQYSNLPTKERLVPREVPRRV
INAININHEFDLLDVRFHELGDVVDVFIIIDDADEIPARDGVFLKLIDGWTEPFAPHMRKSL
PGGRQDGWIADDYLRTFLTQDGVSRLRNLRPDDVIIDDADEIPARDGVFLKLIDGWTEPFAPHMRKSL
YGFFWKQPGTLEVSGCTMDMLQAVYGLD GIRLRRRQYYTMPNFRQYENRTGHILVQWSLGSPLHFAGWH
CSWCFTPEGIYFKLVAQNQDFPRWG DYEDKRDLYI RSLIRTGGWF DGTQQEYPPADPSEHMYAPKYLL
KNYDQFRYLL ENPYREP KSTVEG GRQNQGSDGRSSA VRG KLD TAE G

10/500240

FIGURE 33

>gi|6912501|ref|NM_012214.1| Homo sapiens mannosyl
(alpha-1,3-) -glycoprotein beta-1,4-N-
acetylglucosaminyltransferase, isoenzyme A (MGAT4A), mRNA

GAAATGAACCTCTTATTGATTGGCTAGAGCCAGGAGTACTGCATTGACTTCAGG
GTAAAAAGAAAACAGTCTGGTGTCACTATAAACATATGGACCAGTGTATGGTAAATGAGATG
AGGCTCCGCAATGAACTGTAGCCACTGCTTAGCATTATCACTTCCTCCTACTTTGTCTGGTAT
ACTACATGGCAAAATGGGAAAGAAAAACTGATTGCTTATCAACGAGAATTCTTGCTTGAAGAACGT
CTTCGAATAGCTGAACACAGAACATCTCACAGCCTCTGAATTAAATACGATTGTGCAACAGTCAAG
CGTGTAGGAGCAGAAACAAATGGAAGTAAGGATGCGTTGAATAAGTTTCAGATAATACCTAAAGCTG
TTAAAGGAGTTAACAGCAAAAATCTCTCAAGTCCAAGTATTATTATCATTGCTCATTATTG
AAAAATGAAGGAAGTCTCAACCTGCTGTACAGATTGGCAACGGAAGAACAGGAGTTCAATAGTCATG
GGCATTCCCACAGTGAAGAGAGAACATCTTACCATAGAAACTCTCATTCCATTGATAAC
CTGTATCCTGAAGAGAAGTGGACTGTGTTAGTAGCTTCATAGGAGAGACAGATATTGATTATGTA
CATGGTGTGTTAGCCAACCTGGAGAAAGAATTTCTAAAGAAATCAGTCTGGCTTGGTGAAGTCATA
TCACCCCCCTGAAAGCTATTATCCTGACTTGACAAACCTAAAGGAGACATTGGAGACTCCAAAGAAAGA
GTAAGATGGAGAACAAAGCAAAACCTAGATTACTGTTCTAATGATGTATGCTCAAGAAAAGGGCATA
TATTACATTCACTGAAGATGATATTATTGCAAACAAAATTATTTAATACCATAAAAATTGCA
CTTCACCTTCTTCTGAGGAATGGATGATTCTAGAGTTTCCAGCTGGCTTCAAGTAAATGTT
CAAGCGCCGATCTTACTCTGATTGAGAATTCAATTCATGTTTACAAGGAGAACCCATTGATTGG
CTCCTGGACCATATTCTCTGGGTGAAAGTCTGCAACCTGAAAAGATGCAAAACATTGATAGACAG
AAAGCAAATCTCGAATTGCTTCAGACCTCCCTTCCAACATGTTGGTCTGCACTCATCACTATCA
GGAAAAATCCTAAACACTCACGGATAAAGATTATGAAACCATTACTTCTAAATCCATGTAACCCA
CCTCGGGAGGTATCTACTCCCTGAAAGGTCTACCAAGGGCATACTGGAGAAAACCTACATGGAGAG
GATTCTCTGGCTATCACACCGATAGCTGGAGACTACATCTGTTAAATTGATAAACCACTGCAAT
GTAGAAAGTTATTGTTCCATAGCGGCAACCAAGAACATCCTGGAGATATTCTGCTAACACAACTGTG
GAAGTTTGCTTTAAGAGTGAAGGTTGAAATAAGCAAAGAACCAAACGATTAGAAGAT
GGCTATTCAGAAATAGAAAATTGAGAATGGTGTGAGAAGGAATGGTGGATCCAAGTCTCAATCCC
ATTTCAGCCTTCGACTTCACTGTTTCAAGATTCTGCTGTTGGCATTCTTAATGAGATTCAATT
AAAAAGCCACCAACTGATCATCTGAGAAACCAACACATTCTGTGAATTGTTAATTAAAGATA
GTTAAGCATGTATCTTTTTATTCTACTTGAAACACTACCTCTGTGAAGTCTACTGTAGATAAGAC
GATTGTCATTCCACTGGAAAGTGAATCTCCATAATAATTGTTGTTGAAACTAAGCTGCTC
AGATTTAACTGACTCAAACATTTCATTGACAGCCTGTTAATATGACTTGTACTATTGGTA
TTACTAATACATAAGAGTTGACATTGTTACATTCTTAAATTGAGAAAACATAATGTTACATA
CATTTATGAAGGGGTACTTTGAGGTTCACTTATTACTATT

>gi|6912502|ref|NP_036346.1| mannosyl (alpha-1,3-) -
glycoprotein beta-1,4-N-acetylglucosaminyltransferase,
isoenzyme A; UDP-N-acetylglucosamine:alpha1,3-d-mannoside
beta1,4-N-acetylglucosaminyltransferase; alpha-1,3-
mannosyl-glycoprotein beta-1,4-N-
acetylglucosaminyltransferase [Homo sapiens]

MRLRNGTVATALAFITSFLTLSWYTTWQNGKEKLIAYQREFLALKERLRIAEHRI
RSSELNTIVQQFKRVGAETNGSKDALNKFDNLTLLKELTSKKSLQVPSIYYHLPH
LLKNEGSLQPAVQIGNGRTGVSIVMGIPTVKREVKSYLIETLHSЛИDNL
VIVVFIGETIDYVHGVanLEKEFSKEISSGLVEVISPPESYYPD
LNLKETFGDSKERVRWRTKQNLDYCFMMYAQEKGIYYIQLEDDIIVK
QNYFNTIKNFALQLSSEEW
MILEFSQLGFIGKMFQAPDLTIVEFIFMFYKEKPIDWL
LHDHILWVKVCNPEKDAH
CDRQKANLRIRFRPSLFQHVGLHSSL
SGKIQKLTDKDYMKPLLKIHV
NPPAEVSTS
LK
VYQGHTLEKTYMGEDFF
WAITPIAGDYILFKFDKP
VNVESYLFHSGNQEHPGDIL
LNTTVEVLPFKSEGLEIS
KETDKRLEDGYFRIGKFENG
VAEGMVDP
SLNP
ISAFRL
SVIQNSAVWAILNEIHI
KKATN

FIGURE 34 (sheet 1)

>gi|18997006|gb|AF474154.1| Mus musculus N-acetylglucosaminyltransferase V (Mgat5) mRNA, complete cds

ATGCTAGAGAGAGATGGCTTCTTTCTCCCTGGAAGTTGTCCCTCTCAGAAGCTGG
 GCTTTTCTGGTACTTCGGCTTCATCTGGGCATGATGCTCTGCACCTCACCA
 TCCAGCAGCGGACTCAGCCGAGAGCAGCTCCATGTTACGGGAGCAGATCCTGACC
 TCAGCAAGAGGTACATTAAGCACTGGCAGAGGAGAACAGGGACGTGGATGCC
 CCTACGCTGGTGTATGACAGCCTATGATCTGAAGAAAACGCTGCCGTCTGCTGG
 ATAACATCCTGCAGCGCATTGGCAAGCTCGAGTCAAAGGTGGACAATCTGGTCAACG
 GCACAGGAGCGAACTCCACCAACTCCACACGGCTGCCCCAGCTGGTGTGCTTG
 AGAAAATTAATGTGGCAGATATCATTAATGGAGTTAGGAAAAATGTGTATTGCC
 CTATGGATGGCTACCCCCACTGCGAGGGAAAATCAAGTGGATGAAGGACATGTGGC
 GCTGGACCCCTGCTACGCAACTATGGAGTGGACGGACCTCTGCTCCTTTTA
 TTTACCTCAGTGAGGTTGAAAATTGGTGTCTCGTTACCTGGAGAGCAAAAATC
 CCTATGAAGAAGCTGATCATAACTCATTGGCGGAAATCGTAGGGATTAAACATT
 TCTACGGCATGATGAAGAACGACGAGGAGITCCGTTGGATGAGGCTCGGATCCGGC
 GAATGGCTGACCGTGGATCCAAGCTATCAAGTCTCTGGCGGAGAAACAAAACCTG
 AGAAGAGGAAACGGAAGAAAATCCTGTTACCTGGGCTCTGACCAAGGAATCGG
 GCTCAAGATTGCGGAGACAGCATTGCGGTGGCCCTCTGGGTGAACTCGTTAGT
 GGAGTGACTTAATCACATCTGTACCTGCTGGGCCATGACATCCGGATCTGGCCT
 CACTGGCTGAGCTCAAGGAGATAATGAAGAAGGTTGGAAACCGGTCTGGCTGTC
 CAACTGTAGGAGACAGAACGAGCTGATTATATCGATATTGTGGACTTGCTC
 AATTAAAGAAAACACTAGGGCCATCCTGGGTCATTACCAAGTGCATGCTCCGGGTC
 TAGACTCCTTGGAACAGAACCTGAGTTCAATCATGCGAGCTATGCCAGTC
 AAAAGGCCACAAGACCCCTGGGAAAGTGAATCTGAACCCGAGCAGT
 TTTACCCATCACACAGCTTCTGGCTCGTGGAGCAGCACCTGA
 ACTCCAGCGACATTCAACCACATCAACGAGATCAAAGGCAGAAC
 CCAGTCCCTGTGATCTGGGCTCGGATTCCCTATGAAGGCCCAGCT
 CCCCTGGAGGCCATCGGAAAGTGGATGTGCTTCTCAACACCG
 ACTGAACTGCAAGGAGACAGCTGAGAGAGCTGACATCCCAGC
 ATCCTTACAGGAGACAGCTGAGAGAGCTGAGAGAG
 AAGTGAAGATGCAGTAAAGCCATCTAAACAGAAGATTGAGCGT
 ATGAGTTACATGTGAAGGCATGCTGCAGAGAACGCTTCAATT
 GAAAACAGG
 ACTTCTGCCATGGCCAAGTGAATGTGGCCGCCCTCAGCGCC
 CTGAGCCAGGGCAGTCCTGCAAACAGGTGTGCCAGGAGAG
 CCAGCTCATCTGGCTCGTGGACTTCAGTGTGCGGAGGCC
 CATCCCTTCAACACCTCAACAAAGGAAAAGGAC
 CTGCTGAAGTATAAGGTGACCT
 GCCAAAGCTCAGAACACTGTACAAGGACATCCTGG
 CTGAGCCAGGGCAGTCCTGCAAACAGGTGTGCCAGGAGAG
 CCAGCTCATCTGGCTCGTGGACTTCAGTGTGCGGAGGCC
 CATCCCTTCAACACCTCAACAAAGGAAAAGGAC
 CTGCTGAAGTATAAGGTGACCT
 GCCAAAGCTCAGAACACTGTACAAGGACATCCTGG
 CTGAGCCAGGGCAGTCCTGCAAACAGGTGTGCCAGGAGAG
 CCAGCTCATCTGGCTCGTGGACTTCAGTGTGCGGAGGCC
 CATCCCTTCAACACCTCAACAAAGGAAAAGGAC
 CTGCTGAAGTATAAGGTGACCT
 ACTGGGCAGGGCCAAGGGCACAAAGACATT
 CAGGGACTCTGACCGAGCAGCCTGAG
 ATCTGGTCCAGGGCTTGAGTTAGTACCGCTCCAG
 CCACAGCCAGTGCATCCCAGTT
 TACACCAAAACCACAAGGAA
 ACAGGTTAGAACAGGAAC
 CTGGGTTCTCCTCAGTGT
 AGGAATGTCTCTGTCTGGAGATCGAGCGACTGT
 AGGGAAAGGATCCAGGCA
 GTTGCTCCGGAGAC

10/500240

FIGURE 34 (sheet 2)

TCATTCAAACGTAAAACAGGAAGAGGGATTGAGCCAATTGGGAAGGACTTT
GGGGCCGATCCTAAACCAATTAAATTATTTGGGAGGGATGGGGCGGGCTCGGG
AGGGAGGGAGAGGGGTTAACAGTTCCTTGTTCCTCACTGTTAATTGCCACCT
TCGGGCCCTTCTTGTCTGCAGCGCCAAGCAGGGTGAGAGGGCTGTGGCTTGCCT
GAGGGGCCACTGTGGGCTTCACTCCTGGTCACAGGTGGCAGCAGAGAAAAGAGATG
TCTATAAGCAGGGGATGTAGCTCAGTTGAGAATGCTGCATAGCATAATGAAG
TCCTGGGTTCCATCCCCAGCACACATAAAATGCAGGTAAAGAAACAGAGTCAGGAGGA
CCAAGCATTCTCCTTGGCTACATAACAAAAGCAAGGCCTTGTCCCCATGTCTTGGC
TACAAGAGACCCATCTCAGAAAATTGTGGGGGAGGGGGGGAAATGGCCTTGA
AAACACAGCCAGTCACTGCACTGCCAGAACTGGTGGATCCCAGGTGTGCTT
GGCAGATAACAGCTAAAGGCACATAACCTGGTGGGAAATAATGCCTGTGGTGT
CCTGAGGGCCCCACCAAGTCCAAAAAA

>gi|18997007|gb|AAL83249.1|AF474154_1 N-
acetylglucosaminyltransferase V [Mus musculus]

MAFFSPWKLSQKLGFVTFGFIWGMMLLHFTIQQRTQPESSSMLREQILDLSKRY
IKALAEENRDVVDGPYAGVMTAYDLKKTAVLLDNILQRIGKLESKVDNLVNGTGAN
STNSTTAVPSLVSLEKINVADIINGVQEKCVLPPMDGYPHCEGKIKWMKDMWRSDPC
YADYGVDTSCSFFIYLSEVENWCPRLPWRAKNPYEEADHNSLAEIRTDNFNILYGM
KKHEEFRWMRLRIRRMADAWIQAISLAEKQNLEKRKRKKILVHLGLLTKESGFKIA
ETAFSGGPLGELVQWSDLITSLYLLGHDIRISASLAELKEIMKKVVGNRSGCPTVGD
RIVELIYIDIVGLAQFKTLGPSWVHYQCMLRVLDSFGTEPEFNHASYAQS
KGHKTPWGKWNLNPQQFYTMFPHTPDNSFLGFVVEQHLNNSDIHHINEIKRQNQSLVYGV
DSFWKNKKIYLDIIHTYMEVHATVYGSSTKNIPSYVKNHGILSGRDLQFLLRETKLV
FVG LGFPYEGPAPLEAIANGCAFLNPKFNPPKSSKNTDFIIGKPTLRELTSQHP
YAEVFI GRPHVWTVDLNNREEVEDAVKAILNQKIEPYMPYEFTCEGMLQRINA
FIEKQDFCHG QVMWPPLSALQVKLAEPGQSKQVCQESQLICEPSFFQHLNKE
KEDLLKYKVTCQSSE LYKDILVPSFYPKSKHCVFQGDLLFSCAGAHPTHQR
ICPCRDFIKGQVALCKDCL

**This Page is Inserted by IFW Indexing and Scanning
Operations and is not part of the Official Record**

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images include but are not limited to the items checked:

- BLACK BORDERS**
- IMAGE CUT OFF AT TOP, BOTTOM OR SIDES**
- FADED TEXT OR DRAWING**
- BLURRED OR ILLEGIBLE TEXT OR DRAWING**
- SKEWED/SLANTED IMAGES**
- COLOR OR BLACK AND WHITE PHOTOGRAPHS**
- GRAY SCALE DOCUMENTS**
- LINES OR MARKS ON ORIGINAL DOCUMENT**
- REFERENCE(S) OR EXHIBIT(S) SUBMITTED ARE POOR QUALITY**
- OTHER:** _____

IMAGES ARE BEST AVAILABLE COPY.

As rescanning these documents will not correct the image problems checked, please do not report these problems to the IFW Image Problem Mailbox.